

# STIC Search Report Biotech-Chem Library

# STIC Database Transing North

TO: Nita M Minnifield

**Art Unit: 1645** 

Location: rem/3C01/3C18 Serial Number: 09/970076

Friday, June 17, 2005

From: Beverly Shears

**Location: Biotech-Chem Library** 

**REM 1A54** 

Phone: 571-272-2528

beverly.shears@uspto.gov

## Sealer Voices

### **Protein Sequence Searches – February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.



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ALIGNMENTS

### RESULT 1 ABP54903 ID ABP5 XX ABP5 XX ABP5 XX Huma XX Huma XX Anth XX Anth XX Anth XX PT Pept FT Regi FT Doma FT Regi FT Doma Domain Domain Region Region Region Region Domain Region 08-JAN-2003 ABP54903; Region Domain Protein Peptide Homo sapiens Anthrax; toxin; Human anthrax toxin receptor. ABP54903 standard; protein; (first receptor; human; antibacterial. note= "putative transmembrane 344. 368 /note= "forms metal ion-dependent amotif with amino acid residues 50, /note= "forms metal ion-dependent amount with amino acid residues 50, /note= "forms metal ion-dependent adhesion motif with amino acid residues 50, 54, 118 /note= "forms metal ion-dependent adhesion motif with amino acid residues 52, 54, 118 /note= "PA-binding fragment, begins at any amino acid in the range 27-43 and ends at any amino acid in the range 221-321, region specifically described in Claim 3" /label= Signal\_peptide 27. .321 /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 52, 54 and 150" Location/Qualifiers 'note= "von Willebrand factor A domain" note= "extracellular domain" label= Mature\_protein .368 entry) "cytoplasmic domain" 368 B domain" adhesion 52, 118 adhesion site (MIDAS), 52, 54 and 118" site (MIDAS) and 150" site (MIDAS) and 150" site (MIDAS) and 150"

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 Human;
                              Human gene 4 encoded secreted protein HWLFR02,
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100.0%; Pred. No. 1.
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CA AADD5300-AADD5379 represent cDNAs corresponding to 28 human secreted comprotein genes, and AAE0146-AAE01513 represent the proteins they encode. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating correct on the first protein or gene therapy. CC pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 28 genes, common the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune cd diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune cognitive disorders, diseases of the immune system, AIDS, autoimmune cognitive disorders, disbetes, atherosclerosis, cardiovascular disorders, candiopenia, asthma, skin disorders, (e.g., prepinancy-related disorders, atherosclerosis, cardiovascular disorders, candiopenic disorders, atherosclerosis, cardiovascular disorders, prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding protein of the invention can be used as a food additive or greservative to modify storage properties. Antibodies specific for a grotein of the invention can be used in alleviating symptoms associated could protein of the invention can be used in alleviating symptoms associated could protein of the invention can be used in alleviating symptoms associated could protein of the invention can be used in alleviating symptoms associated could protein of the invention and human secreted protein of the invention can be used in alleviating symptoms associated could protein of the invention can be used in alleviating symptoms associated could protein of the invention can be used in alleviating symptoms associated could be composed to the inv
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30-JUN-2000; 2000US-0215133P.
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The present invention relates to albumin fusion proteins comprising a therapputic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapputic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders
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                                                                                                                                                                                                                                       12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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HASELTINE W A.
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albumin fusion proteins,

useful for diagnosing, treating,

preventing

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activities: cyrostatic, antianaemic, antiarthritic, antiasthmatic, anti-
CC HIV, immunosuppressive, antiinflammatory, antipsoriatic, antibacterial,
CC osteopathic, dermatological, antigout, immunomodulator, antiarrhythmic,
CC cardiant, nootropic, antilipaemic, nephrotropic, uropathic,
CC cardiant, nootropic, antiparkinsonian, tranquilizer, antidiabetic, anabolic,
CC hypertensive, and vulnerary. The albumin fusion protein nucleic acid may
CC he used in gene therapy to treat disorders. The albumin fusion protein is
CC useful for diagnosing, treating, preventing or ameliorating diseases or
CC disorders comprising indication: Y. The diseases or disorders include:
CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer)
CC immune or haematopoletic diseases (e.g. anaemia, Hodgkin's disease, acute
CI lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,
CC autoimmune disease, inflammatory bowel disease, scutes
CC disease), reproductive system disorders (e.g. prostatilis, inguinal
CC leydig tumours), musculoskeleletal diseases (e.g. giant cell tumours,
CC disease, exertenic lunus ervitematorus
CC disease, acute controlled disease (e.g. giant cell tumours)
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Best Local S
Matches 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein and its compositions have the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 albumin fusion protein formula; a method of treating a disease or disorder in a patient comprising the step of administering the albumin fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of extending the shelf life of Therapeutic protein: X, or its a method of extending the shelf life of Therapeutic protein: X, or its
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98

TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120

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   Matches 295;
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Best Local
                                                                                                                                                                                                                                                                                     The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90730, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour provent, neosangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL93096-ABL93041 and ABL92143-ABL93191; normal and other of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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11-APR-2001; 2001US-0282850P
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polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
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                                       Similarity
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                                                                                                                                                    564 AA;
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   Conservative
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                                       Score 1536; DB 5
Pred. No. 3e-156;
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11-AUG-2000;
11-APR-2001;
                                       The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90730, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenic activity bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                                                    An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis.
                                                                                                                                                                                                                                                      Disclosure; Page 136-137; 331pp; English
                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-291856/33.
                                                                                                                                                                                                                                                                                                                                                                                      St Croix B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-2001; 2001WO-US024031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mouse; rat; TEM; tumour endothelial marker; normal endothelial marker; pan-endothelial marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Tumour
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2000US-0224360P.
2001US-0282850P.
                                                                                                                                                                                                                                                                                                                                                                                      Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                                     JOHNS HOPKINS
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Query

Match

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Claim 1; Page 37-39; 45pp; English

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RESULT 7
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                                                                                                        Novel isolated polypeptide useful for identifying agent that prevents or reduces effect of anthrax toxin on host cell, for treating human or non-
                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2001; 2001WO-US030941
                                                                               human
                                                                                                                                                                                                                                                               Young JAT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human anthrax toxin receptor.
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                                                                             animal suffering
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                                                                                                                                                                                                                                                                                                                                                                                                 Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; nem; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; necangiogenesis; immune response; cytostatic; antidiabetic;
   11-APR-2001;
06-FEB-2002;
                                                                                                    10-APR-2002;
                                                                                                                                                                      24-OCT-2002
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                                                                                                                                                                                                                                                                                                       Homo sapiens
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Pred. No. 3e-156;
Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a novel method for the isolation of endothelial cells (ECS), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are all useful for inhibiting meoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                             neoangiogenesis; i
ophthalmological;
                                                              pan-endothelial marker; polycystic kidney disease;
diabetic retinopathy; rheumatoid arthritis; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 564 AA;
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                                                                                                                                            Human tumour endothelial marker TEM
                                                                                                                                                                           12-MAR-2003
                                                                                                                                                                                                          ABU54431;
                                                                                                                                                                                                                                        ABU54431
                                                                                               Tumour
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                                                                                             endothelial cell; EC; tumour endothelial cell;
endothelial marker; normal endothelial marker;
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                                               immune
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                                immune response; cytostatic; antidiabetic;
antirheumatic; antiarthritic; antipsoriat
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Pred. No. 3e-156
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angiogenesis;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoanglogenesis or tumour anglogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
                Human heat mitochondrial protein as
                                               06-MAY-2004
                                                                                                          ADJ70017 standard; protein; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 564 AA;
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06-FEB-2002; 2002US-0354262P
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                                                                                                                                                                                       LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS
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Pred. No. 3e-156;
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              a therapeutic target SeqID1823.
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17-JUN-2002;
20-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHOM), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nottropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic activities. This polypeptide sequence mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function,
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ALQGIHSILKKSCIBILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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2002US-0389987P.
2002US-0412418P.
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                                                                                                                                                                   The present invention describes a method for detecting a pancreatic CC cancer-associated transcript in a biological sample. The method comprises CC contacting the biological sample with a polynucleotide that selectively CC hybridises to a sequence at least 80% identical to a sequence as shown in CC any one of Tables 3 to 25 in the specification or having the GenBank CC cancer in a human or animal subject being tested, determining the CC likelihood that a subject having a pancreatic cancer will survive, or CC determining the suitability of a subject having a pancreatic cancer will survive, or CC surgical resection therapy; (2) detecting a pancreatic cancer for CC surgical resection therapy; (2) detecting a pancreatic cancer associated CC subject having a pancreatic cancer will survive; and (4) monitoring the CC efficacy of a therapeutic treatment of pancreatic cancer. A pancreatic cancer associated transcript has cytostatic activity, and can be used in CC gene and protein therapy. A pancreatic cancer cancer. A pancreatic concer-associated polypeptide or an antibody that binds to the isolated polypeptide can be used for diagnostic methods are useful for the polymcleotide, a vector comprising the polymcleotide, an isolated concer or its metastases, and for monitoring the progress of disease such as during remission or following surgery or chemotherapy. The present CC cancer remission or following surgery or chemotherapy. The present CC sequence represents human tumour endothelial marker 8 precursor (TEM8), which is used in the exemplification of the present invention.
Query Match
Best Local S
Matches 295
                                                                                                                          Sequence
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   Score 1536; DB 8
Pred. No. 3e-156;
Mismatches 0
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The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig mutated fusion protein of the invention.

Claim 45; SEQ

IJ

NO 18;

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English

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                                                                                                                                                                                                                                                                                                                                                         New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-liked domain (VWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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HEALEY J J.
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O'KEBFE T L.
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Best Local
                                                                                                                                                      ameliorating domain (vWF) to the vWF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
vWF amino acid sequence; TANGO197; immunoglobulin; Ig; fusion protein;
                                                                                                                                                                           New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing ameliorating symptoms of anthrax comprises a von Willebrand factor domain (vWF) amino acid sequence and an amino acid sequence hetero
                                                                                                                                                                                                                                                                             WPI; 2003-829643/77.
N-PSDB; ADM64575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence hetarologous to the vWF. Also described are: a method of preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROTT/)
                                                                                               Claim 44; SEQ ID NO 18; 64pp; English.
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HEALEY J J.
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Pred. No. 7.8e-156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;
                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ameliorating a symptom of anthrax in a subject thought to be at risk f exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypepti. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino aci sequence of a fusion protein comprising mouse TANGO197 and immunoglobu (Ig) that can be used to treat exposure to or prevent a symptom of
                                                                                                                                                                                                          Misc-difference
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Pred. No. 7.8e-156;
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CC AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating cor ameliorating medical conditions, e.g., by protein or gene therapy. CC Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 28 genes, the new genes. Specific uses are described for each of the 28 genes, CC based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune cdisorders, cancer, tumours, foetal and developmental abnormalities, autoimmune disorders, cancer, tumours, foetal and developmental abnormalities, cognitive disorders, ecf., Alzheimer's disease, Parkinson's disease), CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g., Parkinson's disease), CC angiogenic disorders, kidney disorders, gastrointestinal disorders, gregnancy-related disorders, endocrine disorders, and infections. The CC proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc protein of the invention can be used in alleviating symptoms associated corrected of the invention can be used in alleviating symptoms associated corrected to the invention of the
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D; Mismatches 2;
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Query Match Best Local Matches 293;

Similarity

99.2**%**; 99.3**%**;

Score 1524; Pred. No. 3.

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                                                       The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, reproductive disorders (e.g. Alzheimer's, enhizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Albumin fusion protein; therapeutic protein; human albumin; lhuman serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder;
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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	SVIITTTHCSDXS 321	SVIITTHCSDGS 295	ARNVDRVLCSFKINDSVT	ARNVDRVLCSFKINDSVT	ARIADSKDHVFPVNDGFQ	ARIADSKDHVFPVNDGFQ	EQIYYENRQGYRTASVII	EQIYYENRQGYRTASVII	LAHKFISPQLRMSFIVFS	LAHKFISPQLRMSFIVFS
			266	240	206	180	146	120	86	60

Search completed: June 13, 2005, 19:56:46 Job time: 111.221 secs

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2: uniprot_trembl:*
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Copyright (c) 1993 - 2005 Compugen Ltd
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  99cz52

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08t5c2

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3 mytilus edu
5 homo sapien
6 yallus gall
7 homo sapien
8 yallus gall
8 mus musculu
1 eimeria max
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6 homo sapien
7 rattus norv
9 homo sapien
8 halocynthia
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mytilus edu
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SEQUENCE OF 184-564 PROM SEQUENCE OF 184-564 PROM SEQUENCE OF 18702039; DOI=10. Ota T., Suzuki Y., Nishi Wakamatsu A., Hayashi K., Sekine M., Obayashi M., Yamamoto J.I., Saito K., Nagahari K., Murakami K., Shiratori A., Sudo H., H Sugawara M., Takahashi M. Omura Y., Abe K., Kamiha Yamazaki M., Ninomiya K. Fujimori K., Tanai H., Yahida S., Ono Y., Takig Kusano J., Kanehori K., Nomura Y., Togiya S., Ko Imose N., Musashino K. Yoshikawa Y., Matsunawa Moriya S., Momiyama M., Nakagawa S., Senoh A., M Hishigaki H., Watanabe T. Yamazaki M., Watanabe T. Yamazaki M., Watanabe T. Yamazaki M., Watanabe T. Chirani P. Kawabata A., Hikiji T., Okirani P. Kawabata T., Okirani P. Kawabati T.,	LIT 1  LHUMAN  ATRI HUMAN  ATRI HUMAN  STANDARD;  Q9H6KZ; Q9SED2; Q9NVP3;  28-FEB-2003 (Rel. 41, Last;  05-UUL-2004 (Rel. 44, Last;  05-UUL-2004 (Rel. 44, Last;  Anthrax toxin receptor 1 pri Name=ANTRI; Synonyms=ATR, '  Homo sapiens (Human).  Eukaryota; Metazoa; Chordat;  Rumanlia; Eutheria; Primate;  NCBI_TaxID=9606;  [1]  SEQUENCE FROM N.A. (ISOFORM  MEDLINE=20407466; PubMed=10.)  SEQUENCE FROM N.A. (ISOFORM  MEDLINE=21597240; PubMed=11.)  Bradley K.A., Mogridge J., 1  "Identification of the cell:  Nature 414:225-229(2001).	123 121 121 121 120.5 118.5 118.5 118.5 118.5 118.5 118.5
OF 184-564 FROM 3) 4702039; DOI=10 Suzuki Y., Nishi u A., Hayashi K. i, Obayashi M. ii, Ninomiya K. Kamhashi H. ii, Ninomiya K. Kamehori K. ii, Tanai H. ii, Ono Y. Takig ii, Tayai K. ii, Tayai K. ii, Kanehori M. ii, Matanabe T. ii, Komiyama M. yamada K. Y. Komiyama M. yamada K. Y. Kanakami T. p. Kanakami T. p. Kanakami T.	WAN STANT 096PD2; QNV 2003 (Rel. 41 2004 (Rel. 4	777777777778 66677777788990
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EQUENCE FROM N.A.  Yama T., Irie R.,  Tanaka T., Ishii S.,  kamura Y.,  Kamura Y.,  Kamura Y.,  Kamura T., Kikkawa E.,  K., Tanikawa M.,  K., Tanikawa M.,  K., Tanikawa K.,  Iraoka S., Chiba Y.,  Iraoka S., Chiba Y.,  Sida M., Hotuta T.,  H., Tanase TO.,  I K., Arita M.,  Sida M., Aotsuka S.,  a N., Sano S.,  aki N., Aotsuka S.,  aki N., Aotsuka S.,  aki N., Wakebe H.,  M., Kawakami B.,  Fukuzumi Y.,  M., Kawakami B.,  Fukuzumi Y.,  Johmori Y., Okamoto S.,  Irema Y., Okamoto S.,  Incra K., Senba T.	e) ndothelial marker 8). tebrata; Euteleostomi; ominidae; Homo.  126/science.289.5482.1197; so G., Romans K.E., er C., Vogelstein B., ."; TION WITH ANTHRAX TOXIN. 038/n35101998; 038/n35101998; er R.J., Young J.A.T.; r anthrax toxin.";	O9ji30 rattus norv O6mg73 rattus norv O8cip8 rattus norv O7rf52 plasmodium O6dcq6 xenopus lae O8cbt2 mus musculu O75r52 lymnaea sta O9es77 mus musculu O75r52 bos taurus O91145 notophthalm O8ivxl homo sapien O6pi59 homo sapien O9p218 homo sapien

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Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Balkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Bothersh A., Schein J.E., Jones S.J. M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human of the company of the company
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Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Yamashita R.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Okumura K., Nada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100; Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH ANTHRAX
                                                                                       TISSUE SPECIFICITY: Highly expressed in tundut not in normal endothelial cells.
DOMAIN: Binding to PA seems to be effected SIMILARITY: Belongs to the ATR family.
SIMILARITY: Contains 1 VMFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms=4; Comment=Experimental confirmation may be la
                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1;
                                                                                                                                                                                                                                                                                                                                           IsoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low levels due to
codon in the mRNA, leading to nonsense-mediated
                                                                                                                                                                                                             IsoId=Q9H6X2-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl.
                                                                                                                                                                                                                                                      IsoId=Q9H6X2-3;
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                                                                                                                                                                                                                                                                                                VSP_000445;
                                                                                                                                                                                                             VSP 000449;
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InterPro; IPR008399; Anth C.
InterPro; IPR008395; VWF A.
Pfam; PF05587; Anth Ig; T.
Pfam; PF05586; Anth C; 1.
Pfam; PF00592; VWA; 1.
SMART; SM00327; VWA; 1.
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AF421380;
AK025429;
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                  LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS
                                                                                      ALQGIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                             ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                                                TRGTTLMKLTEDREQIRQGLEELQKVLFGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                                                                                                                                                                                                                                           GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRWSFIVFS
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                                                                                                                                                                                                                TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                                                                                                                                                                                                                       GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
LNEKPFSV
                                                                   ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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BAB15128.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564
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364
368
368
1664
                                                                                                                                                                                                                                                                                                                                                                                                                                 62789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nt is not removed. Use agreement (Sec. 'Sec)
                                                                                                                                                                                                                                                                                                                                                                                                                                 X
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ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                          0
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Cytoplasmic
VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (1)
/FTId=VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform /FTId=VSP_000449. B118A00AD5DF2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (In isoform 2).
/FTId=VSP_000445.
NEKPFSVEDTYLLCPAPILKEVGMKAALQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anthrax toxin receptor 1. Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WVSSTSGFKEGNSHPCLPARPHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asp/Glu-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSILAIALLILFLL -> LHKIASGPTTAACME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP 000444.
Missing (In isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lsoform 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTId=VSP
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nked (GlcNAC. . .) (Potential).
nked (GlcNAC. . .) (Potential).
hked (GlcNAC. . .) (Potential).
-> NKIK (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                         1536; DB 1;
No. 2.4e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (In isoform 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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RESULT 28
ATRI MODE
ATRI ATRI
AC 09023
DT 28-F
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis S.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzieraki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Kedzieraki R.M., King B.L.,
RA MagJott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maggashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylona P.A., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hara A., Hashizame W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Yannishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Sasaki K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Sasaki D., Shibata K., Shinagawa A.,
CC --- SUBUNIT: Binds to the protective antigen (PA) of Bacillus antigen (PA) of Bacillus antigen (PA) of Bacillus antigen (PA) of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-2144368; PubMed=11559528; Carson-Walter E.B., Watkins D.N., NKInzler K.W., St Croix B.; "Cell surface rumon" 1.
                                     This
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 88-562 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer Res. 61:6649-6655(2001).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Antxr1; Synonyms=Atr,
Mus musculus (Mouse).
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05-JUL-2004 (Rel. 44, 1
Anthrax toxin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                          SIMILARITY: Belongs to the ATR family. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms-2.
                                  SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                            IsoId=Q9CZ52-1;
                                                                                                                                                         (BOId=Q9CZ52-2; Sequence=VSP_000450;
dote=No experimental confirmation available;
WAIN: Binding to PA seems to be effected through the VWA
/ Similarity).
            the
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(Rel. 41,
(Rel. 44,
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gnt. It is produced through Bioinformatics and the EN
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            TEMBL
            a collaboration -
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RESULT 3
ATR2_HUMAN
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Best Local S
Matches 291
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InterPro; IPRO08409; Anth Ig.
InterPro; IPR008399; Ant C.
InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF_A.
Pfam; PF05586; Anth Ig; I.
Pfam; PF05586; Ant C. 1.
Pfam; PF00092; VWA; 1.
                                                     ATR2 HUMAN STANDARD; PRT; 489 AA.
ATR2 HUMAN STANDARD;
P58335; Q86UII; Q8NB13; Q96NC7;
28-F2B-2003 (Rel. 41, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Anthrax toxin receptor 2 precursor (Capillary
Name=ANTXR2; Synonyms=CMG2;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
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DOMAIN
                                                   Anthrax toxin (CMG-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF378762; AAL11999.1; -.
EMBL; AK013005; BAB28591.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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by non-profit institutions as l
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                                                                                                                                                                                         LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS
                                                                                                                                                                                                                                          ALQGIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                         ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                                   ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                                                                                                                                                             TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENSQGYRTASVII
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                                                                                                                                                                                                                                                                                                                                                                                             GHGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHRFISPQLRMSFIVFS
                                                                                                                                                                                                                                                                                           ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. . .) (Potential).
GRCINFTRVKSQPAKYPLNNTYHPSSPPPPLYTPPPPAP
HCPPPAFSAFTPPISSPSTLPPPQAPPPNRAPPSRPPP
RPSV -> RFRGWRLTICLGSKHVHPGPHPVCATTARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWFA
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA WMFSSFLERAFQ (in isoform 2).
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Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential
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Extracellular
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                                                              morphogenesis
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RA CLUMECUSIA (C. Mishikawa T., Otsuki T., Sugiyama T., Irie R., RA Ota T., Suzuki Y., Mishikawa T., Otsuki T., Sugiyama T., Irie R., RA Wakamatsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Yamadato J.-I., Saito K., Yasuda T., Iwayanagi T., Wagatsuma M., RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Ra Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., RA Yamazaki M., Ninomiya K., Takiguchi S., Watanabe S., Yosida M., Hotuta T., RA Kusano J., Kanehori K., Takiguchi S., Watanabe S., Yosida M., Hotuta T., RA Kusano J., Kanehori K., Takahashi-Pujii A., Hara H., Tanase T.-O., RA Moriya S., Komai F., Hara R., Takeuchi K., Arita M., RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Oshima A., Sasaki N., Aotsuka S., Momiyama H., Satoh N., Takamai S., Forashima Y., Suzuki O., RA Moriya S., Komiyama H., Satoh N., Takamai S., Forashima Y., Suzuki O., RA Moriya S., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Takimori Y., Watanabe T., Kobatake N., Itakura S., Fukuzumi Y., Okamoto Y., Yamazaki M., Watanabe M., Tahiro H., Tanigami A., Fujiwara T., RA Matumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., RA Mishi H., Watanabe M., Komatsu T., Nakagawa K., RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Takahashi T., Nakamura Y., Ohara O., Isogai T., Sugano S., Takahashi T., Nakamura Y., Ohara O., Isogai T., Sugano S., Makai M., Takama Y., Ohara O., Isogai T., Sugano S., Makai M., Masuho Y., Yamashita R., Makai K., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE-21539596; PubMed=11683410;

Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,

Maxwell S.A., Davis G.E.;

"Differential gene expression during capillary morphogenesis

"Collagen matrices: regulated expression of genes involved in

membrane matrix assembly, cell cycle progression, cellular

differentiation and G-protein signaling.";

J. Cell Sci. 114:2755-2773 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scobie H.M., Rainey G.J.A., Bra
"Human capillary morphogenesis
recentor ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSUE=Placenta
                                                                                                                                                                                                               FUNCTION: Cellular role is not yet known.

SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the following preference: calcium > manganese > magnesium > zinc.

Seems to bind to collagen type IV and laminin.

SUBCELULAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmic
                                                                                                                                                                        reticulum and not at the plasma membrane. ALTERNATIVE PRODUCTS:
                                                                                                                                                      Event-Alternative
                                                                IsoId=P58335-2;
                                                                                                          IsoId=P58335-1;
                       :soId=P58335-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF 78-489 FROM N.A. (ISOFORM 3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                    36:40-45(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM 1), AND
Sequence=VSP_008344,
ental confirmation ava
                                                            Sequence=VSP_008343;
                                                                                                          Sequence=Displayed;
                                                                                                                                                   splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradley K.A., Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100:5170-5174(2003).
                                                                                                                                                      Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION
  44, VSP 008345,
available;
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                               VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver, peripheral blood leukocytes, placenta, skeletal muscie, small intestine and spleen.

DOMAIN: Binding to PA seems to be effected through the VWA domain.

SIMILARITY: Belongs to the ATR family.

SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P58335-4; Sequence=VSP_008346;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in colon, heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK055636;
AK091721;
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                       204
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PF00092; VWA; 1
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157; Conservative
                                                                                                             86
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                                                                                                                         STRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVI
                                                                                                                                                                          GOGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNBIYYFVEQLAHKFISPQLRMSFIVF
  TLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
                                   QALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSV
                                                             IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGF
                                                                                                             SSQATIILPLTGDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQI--QKAGGLKTSSII
                                                                                                                                                        GPGGLLRAQEQPSCRRAFDLYFVLDKSGSVANNWIEIYNFVQQLAERFVSPEMRLSFIVF
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BAC03731.1;
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AAP04016.1;
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                        LAQSCTEILELQPSSVCVGEEFQIVLSGRGFMLGSRNGSVLCTYTVNETY
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                                                                                                                                                                                                            51.5%;
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                                                                                                                                                                                                  Score 790.5; DB 1
Pred. No. 8.9e-55;
4; Mismatches 81
                                                                                                                                                                                                                                                                                                   /FTId=VSP_008344.
Missing (In isofo
/FTId=VSP_008345.
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TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Anthrax toxin receptor 2. Extracellular (Potential)
                                                                                                                                                                                                                                             /FTId=VSP_008346.
P -> A (in Ref. 3;
B9F679DB75B6E2B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
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ed (GlcNAc...) (
g (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Signal; Transmembrane.
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                                                                                                                                                                                                                                                                                                               isoform 3).
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CRC64;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Gouellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
VIllalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-Zuu, EMBL; BC076595; AAH76595.1; -.
EMBL; BC076595; AAH76595.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008400; Anth Ig.
InterPro; IPR008399; Ant C.
InterPro; IPR008399; Ant C.
InterPro; IPR008399; Ant C.
InterPro; IPR008399; Ant J.
                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6DFX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF05587; Anth Ig; Pfam; PF05586; Ant C; 1. Pfam; PF00092; VWA; 1.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6; TISSUE=Eye;
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LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                                               EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHED
                                                             GDRYKIGKGLEDLKAVKPVGETYIHEGLKLANEQI--QNAGGLKASSIIIALTDGKLDGL
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Pred. No. 3.
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RESULT REPORT OF THE PROPERTY 
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   sequencing property sequencing property [6]
               STRAIN-C57BL/6J; TISSUB-Testis;

STRAIN-C57BL/6J; TISSUB-Testis;

MEDILINE-20530913, PubMed-11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka T., Tashiro H., Itoh M.,

Shibata K., Itoh M., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM NO. STRAIN=C57BL/6J; TISSUB=Testis;
STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Carninci P., Shibata Y., Hayatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDN
"Normalization and subtraction of rapid discovery of
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The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome k
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical proline-rich reg:
Willebrand factor type A domain containing protein, full insert
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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Mammalia; Eutheria;
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RA Pukuda S., Furuno M., Haragaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hirawoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RI Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR GO; GO:0016021, C:integral to membrane; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
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O96EC6;
O1-DEC-2001 (TrEMBLrel. 19,
O1-DEC-2001 (TrEMBLrel. 19,
O1-OCT-2003 (TrEMBLrel. 25,
ANTXR1 protein (Fragment).
Name=ANTXR1;
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STRAIN=C57BL/6J;
Adachi J., Aizawa
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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SMART; SM00327; WWA; 1.
PROSITE; PS50234; VWFA; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 641 AA; 70415 MW
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                              TISSUE=Breast;
MEDLINE=22388257;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
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                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
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42.2%; Pred. No. 7.2e-40;
Live 58; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19,
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                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                         "Cloning of rat alpha D, a novel beta 2 integrin."; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVi
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9QYE7;
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                                                    +
                                                                                                                                                                                                                                                                                                           Gallatin W.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Breast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin alpha-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAD RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood (By similarity).

SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

SUBCELIULAR LOCATION: Type I membrane protein (By similarity).

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrin with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.
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                                                                                                                                                                                                                                                                                                                                   VanderVieren M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA; 10453 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor.
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Rodentia;
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95.1%;
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                   Kilgannon P.D.,
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No. 1.9e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEA.
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the European Bioinformatics Institute. The
use by non-profit institutions as a
modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
DOMAIN
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DOMAIN
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Inc alpha; 5.
SMART; SM00327; VWA; 1.
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SIGNAL 1
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InterPro; IPR002035; VWP A.
Pfam; PP01839; PG-GAP; 3.
Pfam; PP00357; Integrin_alpha; 1.
Pfam; PP00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF021334; AAF21241.1; -. HSSP; P11215; 1BHQ.
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                                                                                                                                                                                                    Match
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    212
                                                                               152
                                                                                                                     18
                                                                                                                                                            63;
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00242; INTEGRIN ALPHA;
PS50234; VWFA; 1.
  DPOSLVDPIVQLO
                                   DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
                                                                           DIAFLIDGSG8INQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
                                                                                                                   DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adhesion; Glycoprotein;
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1100
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                                                                                                                                                                             10.4%;
                                                                                                                                                        41;
GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                                                                                                                                                      GFFKR motif.
By similarity.
N-linked (GlcNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
Cytoplasmic (Potential).
FG-GAP 1.
FG-GAP 2.
VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 6.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
FG-GAP 7.
FG-GAP 7.
FG-GAP 7.
FG-GAP 7.
FG-GAP 7.
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:
                                                                                                                                                        Score 159.5;
Pred. No. 0.00
11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There
                                                                                                                                                                             ; DB 1;
.00079;
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                                                                                                                                                                                              Length
                                                                                                                                                                                                                                        CRC64;
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(Potential).
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(Potential).
(Potential).
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(Potential).
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RESULT
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                                                                                                                                                                                                                                                              [5]
INTERACTION WITH VCAM1.
INTERACTION WITH VCAM1.
MEDLINE=99370002; PubMed=10438935;
Wan der Vieren M., Crowe D.T., Hoekstra D., Vazeux R. Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R. Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D. Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D. Grayson M.H., Bochner B.S., Gallatin M.M., Staunton D. Williams Detail Detail Detail Communication of the communication of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAD_HUMAN STANDARD;
Q13349; Q15575; Q15576;
16-OCT-2001 (Rel. 40, Creat
16-OCT-2001 (Rel. 40, Last
05-JUL-2004 (Rel. 44, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                     ++
                                                                                                                                         binding interface between I domain and VCAM-1.";

J. Immunol. 163:1984-1990((1999)).

-i-FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocyrosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99059842; PubMed=9841932;
Grayson M.H., Van der Vleren M., Sterbinsk;
Hoffman P.A., Staunton D.B., Bochmer B.S.;
"alphadbeta2 integrin is expressed on huma:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staunton D.E., Gallatin W.M.; "A novel leukointegrin, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N. MEDLINE-96257236; PubMed=8666289; DOI=10.1016/0378-1119(95)00869-1; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=20187620; PubMed=10722744; DOI=10.1074/jbc.275.12.8959; Mori J.D., Johnson A.K., Dillon J.D.; "Structural and functional characterization of the leukocyte in gene CD11d. Essential role of Spl and Sp3."; J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96111956; PubMed=8777714; DOI=10.1016/1074-7613(95)90058-6; Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ITGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH VCAM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin alpha-D precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (mmunity
from the blood.
SUBUNIT: Heterodimer of an alpha and associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane TISSUE SPECIFICITY: Expressed moderat lines and subsets of peripheral blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an alternative
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171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Med. 188:2187-2191(1998).
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                    AR LOCATION: Type I membrane protein. ECIFICITY: Expressed moderately on myelomonocytic subsets of peripheral blood leukocytes and strong
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed on human eosinophils for vascular cell adhesion mole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation update)
(Leukointegrin alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta
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                                                                                                                          beta subunit.
                                                                                                                                                                                                                                                                                                                                        Vazeux R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene-encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukocyte integrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecule
                                                                                                                                                                                                                                                                                                                    evidence
                                                                                                                                                                                                                                                                                                                                                                    Hoffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                     Alpha-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADB2).
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                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                  P.A.,
                                                  cell
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and strongly on

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GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0016337; P:cell-cell adhesion; NAS.
GO; GO:0007160; P:cell-matrix adhesion; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00357; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U37028; AAB38547.1; -.
EMBL; U40274; AAB60634.1; -.
EMBL; U40275; AAB60635.1; -.
EMBL; U40276; AAB60636.1; -.
EMBL; U40277; AAB60637.1; -.
EMBL; U40277; AAB60638.1; -.
EMBL; U40278; AAB60638.1; -.
EMBL; U40278; AAB60638.1; JOINED.
EMBL; U40278; AAB60638.1; JOINED.
EMBL; U40278; AAB60638.1; JOINED.
EMBL; AF187881; AAF62875.1; -.
HSSP; P11215; 1BHQ.
 DOMAIN
TRANSMEM
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
SIGNAL
CHAIN
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1185; INTEGRINA.

PRINTS; PRO0453; VWFADOMAIN.

SMART; SM00191; Int_alpha; 5.

SMART; SM00327; VWA; 1.

PROSITE; PS00242; INTEGRIN ALPHA; 1.

PROSITE; PS50234; VWFA; 1.

Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
MIM; 60
GO; GO;
GO; GO;
GO; GO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue-specialized cells, including macrophages foam cells within atherosclerotic plaques, and on splenic red pulp macrophages. DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integring with I-domains do not undergo protease cleavage. SIMILARITY: Belongs to the integrin alpha chain family. SIMILARITY: Contains 7 FG-GAP repeats. SIMILARITY: Contains 1 VWFA domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit
   ROT entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EM Bioinformatics Institute. There are no restreprofit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
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1162
85
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Cytoplasmic (Potential).
FG-GAP 1.
FG-GAP 2.
VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 6.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
Potential.
Potential.
Potential.
GPFKR motif.
By similarity.
N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular (Potential)
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(Potential).
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(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration - MBL outstation
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                                                                                           Miyazawa S., Azumi K., Nonaka M.;

"Cloning and characterization of integrin alpha subunits from the resolitary ascidian, Halocynthia roretzi.";

If J. Immunol. 166:1710-1715(2001).

C. -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

C. -!- SIMILARITY: Belongs to the integrin alpha chain family.

EMBL; AB048261; BAB21479.1; -.

REMBL; AB048261; BAB21479.1; -.

RESP; P11215; 1BHQ.

RO; GO:00016021; C:integral to membrane; IEA.

GO; GO:000515; F:protein binding; IEA.

RO; GO:000515; F:protein binding; IEA.

RO; GO:000710; P:cell-matrix adhesion; IEA.

RO; GO:000720; P:integrin-mediated signaling pathway; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                 O9BPQ8
O9BPQ8; PRELIMINARY;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                       Name=HrITGAl;
Halocynthia roretzi (Sea squirt).
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Pyuridae, Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
          PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN
SMART; SM00191; Int_alpha; 5
SMART; SM00327; VWA; 1.
                                                           InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                            TISSUE=Hemocyte;
MEDLINE=21103187; PubMed=11160215;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       Integrin alpha Hrl precursor
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N-linked (GlcNAc...)
N-linked (GlcNAc...)
N-linked (GlcNAc...)
Missing (in Ref. 2).
GHPW -> ATP (in Ref. 2).
U -> A (in Ref. 2).
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Pred. No. 0.
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(Potential).
(Potential).
(Potential).
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  Query Match
Best Local Similarity
Matches 65; Conserv
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Best Local
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InterPro; IPR008985; Cona like.
InterPro; IPR003129; TSP N.
InterPro; IPR003129; VWF A.
Pfam; PF01391; Collagen; 16.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8NFW1;
Q8NFW1;
01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (France).
Alpha 1 type XXII collagen.
Alpha 1 type XXII collagen.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:22989; COL22A1.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005198; F:structural molecule activity;
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPRO08161; Clg_helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Cartilage;
Koch M., Jin W., Ashworth T., Burgeson R.E.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell adhesion; Integrin; Signal; Transmembrane.
SIGNAL 1 30 Potential.
CHAIN 31 1332 integrin alpha Hrl
                                                                                                      PROSITE; PS50234; VWFA; 1. Collagen. SEQUENCE 1626 AA; 16111
                                                                                                                                                                                  PRINTS; PRO0453; VWFADOMAIN.
ProDom; PD000007; Clg_helix;
SMART; SM00210; TSSN; 1.
SMART; SM00327; VWA; 1.
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1332 AA;
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
        Conservative
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A; 145851 MW;
                                                                                                         161115 MW;
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9.7%; Score 148.5; DB
25.4%; Pred. No. 0.0091;
live 45; Mismatches 10
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W; OD9108D2B05CFFAE
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                                             DB 2;
     105;
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     Indels
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                                                      1626;
  41;
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  Gape
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Best Local Similarity
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
Proximal thread matrix protein 1 variant a.
Myrilus edulis (Blue mussel).
Eukaryota, Metazoa; Mollusca; Bivalvia; Pteriomor
Myriloidea; Myrilidae; Myrilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903; Sun C., Lucas J.M., Waite J.H.;
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01-JUN-2002
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EMBL, AP414454; AAL83537.1; -.

GO; GO:0005198; F:structural molecul

InterPro, IPR002035; VWF_A.
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TSSFNKLSKIMENVVKLACM
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                                                           NDGFQALQGI IHSILKKSCI
                                                                                                                VILLTDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-T
                                                                                                                                                                            IIALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 AA; 47543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.6%; Score 148; DB 2; ilarity 25.5%; Pred. No. 0.002; Conservative 46; Mismatches 77
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RESULT Q8T5C3

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01-JUL-1989
01-OCT-1996
                                                                                                                                                                                                                                                                                                 HUMAN
ITAM_F
                         MEDLINE=8831503; PubMed=2457584; Corbi A.L., Kishimoto T.K., Miller L.J., Sp "The human leukocyte adhesion glycoprotein type 3, CD11b) alpha subunit. Cloning, prim to the integrins, von Willebrand factor and J. Biol. Chem. 263:12403-12411(1988).
                                                                                                                                                                                                          01-JII-1989 (Rel. 11, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2094 (Rel. 45, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesic
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SEQUENCE 444
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;
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Eukaryota; Metazoa; Mollusca; Bivalvia;
Mytiloidea; Mytilidae; Mytilus.
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01-JUN-2002
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 SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                            Homo
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GO; GO:0005198; F:structural
InterPro; IPR002035; VWF_A.
Pfam; PF00092; VWA; 2.
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                       (Neutrophil adherence receptor)
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002 (TrEMBLrel. 21, Last s
003 (TrEMBLrel. 24, Last a
thread matrix protein 1b.
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                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                  STANDARD;
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25.5%;
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Pred. No. 0.
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primary structure,
r and factor B.";
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                                                                                Springer T.A.;
                                                                                                                                                   Hominidae;
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SEQUENCE FROM N.A.

MEDLLINE=88257215; PubMed=2454931; DOI=10.1

Arnaout M.A., Gupta S.K., Pierce M.W., Ter

"Amino acid sequence of the alpha subunit

receptor Mol (complement receptor type 3).

J. Cell Biol. 106:2153-2158(1988).
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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0569-2126(98)00093-8;

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Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,

Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,

Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,

Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;

"Cation binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLLNB=96363671; PubMed=8747466; DOI=10.1016/S0969-2126(01)00271-4;
Lee J.O., Banketon L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway fo
                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
MEDLLNB=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DUMMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DUMMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458; DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458, DOI=10.1016/0092-8674(95)90517-0;
MEDLLNB=95171458, DOI=10.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-4838(86)90037-3; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pahl H.L., Rosmarin A.G., "Characterization of the Blood 79:865-870(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adherence receptor indicates homology to integrin proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arna "N-terminal sequence of human leukocyte glycoprotein across species and homology to platelet IIb/IIIa."; biochim. Biophys. Acta 874:368-371(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                    80:631-638(1995).
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promoter of the CD11b gene directs
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myeloid-specific
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, Pierce M.W., Tenen D
the alpha subunit of h
receptor type 3).";
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human leukocyte adhesion
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D.G.;
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Proc. Natl. Acad. Sci. U.S.A. 95.4870-4875 (1998).

-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibringen, factor X and ICAM1. It recognizes P1 and P2 peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxvig C., Springer T.A., a beta-propeller domain in integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98226734; PubMed-9560195; DOI-10.1073/pnas.95.9.4870
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Structure 6:923-935(1998)
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DOMALN: The integrin I-domain (insert) is a VWFA domain with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 7 VWFA domain.

SIMILARITY: Contains 1 VWFA domain.

DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdilb.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                J03925 AAA594911;
J04145 AAA59993.1;
J04145 AAA59993.1;
S52227 AAB24821.1;
S52153 AAB24821.1;
S52154 AAB24821.1;
S52155 AAB24821.1;
S52157 AAB24821.1;
S52159 AAB24821.1;
S52161 AAB24821.1;
S52167 AAB24821.1;
S52167 AAB24821.1;
S52167 AAB24821.1;
S52169 AAB24821.1;
S52170 AAB24821.1;
S52170 AAB24821.1;
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S52175 AAB24821.1;
S52217 AAB24821.1;
S52217 AAB24821.1;
S52217 AAB24821.1;
S52221 AAB24821.1;
S52221 AAB24821.1;
S52221 AAB24821.1;
S52221 AAB24821.1;
S52221 AAB24821.1;
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Best Local
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GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWP_A.
Pfam; PF01039; FG-GAP; 3.
Pfam; PF000357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                 Q8T5C2;
                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota, Metazoa, Mollusca; Bivalvia; Pteriomorph.
Mytiloidea; Mytilidae; Mytilus.
                                                SEQUENCE FROM N.A.
MEDLINE=22313036; PubMed=12425661;
Sun C., Lucas J.M., Waite J.H.;
                        "Collagen-binding matrix proteins byssal fibers.";
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
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                                                                                                NCBI_TaxID=29158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane.
SIGNAL
 iomacromolecules 3:1240-1248(2002)
MBL; AY053391; AAL17974.1; -.
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A=144-345.
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@=143-334.
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26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 145.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                        -GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ
                                     from
                                                            DOI=10.1021/bm0255903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAS
                                                                                                                                                                                                             453
                                     elastomeric extraorganismic
                                                                                                                        Pteriomorphia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1152;
                                                                                                                        Mytiloida;
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Best Local
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ERRATUM.
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Torbi A.L., Ga.
Torbi A.L., Ga.
Torbi A.L., Ga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITAX HUMAN STANDARD; PRT; 1163 AA. P20702; OBIVA6; O1-FEB-1991 (Rel. 17, Created) O5-JUL-2004 (Rel. 44, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Integrin alpha-X precursor (Leukocyte adhesion alpha chain) (Leukocyte adhesion receptor p150, alpha chain) (Leukocyte adhesion receptor p150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005198; F:str
InterPro; IPR002035; 
Pfam; PF00092; VWA; 2
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-8816645; PubMed=3327687;

COTDÍ A.L., Miller L.J., O'Connor K., Larson
"cDNA cloning and complete primary structure
leukocyte adhesion glycoprotein, p150,95.";
EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=ITGAX; Synonyms=CD11C;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                      MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                       SEQUENCE FROM TISSUE-Blood;
                                                                                                                                                                                                                                                                  MEDLINE=90153906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364
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                                                                                                                                                                                                                                  90153906; PubMed=2303426;
L., Garcia-Aguilar J., Sp
structure of an integrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMKLTE--DREQIRQGLEELQKYLPG--GDTYMHEGFERASEQIYYENRQG---YRTASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGHADIA FVFDASSSINANN PNNYQLMKN FMKDIVDR FNKTGPDGTQFAVVTFADRATK
                                                                                                                                                                                                           Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 AA; 48784 MW;
                                                                                                                                                 Garcia-Aguilar J., Springer T.A.;
m. 265:12750-12751(1990).
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                                                                                                                    N.A.
                                                                                                                                                                                                         265:2782-2788(1990)
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25.5%;
                                                                                                                                                                                                                                     integrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 145; DB z; -...
Pred. No. 0.0036;
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                                                                                                                                                                                                                                                    Springer
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e alpha subunit
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GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007155; F:cell adhesion; TAS.
DR GO; GO:0009187; F:organogenesis; TAS.
N InterPro; IPR000413; Integrin_alpha.
R InterPro; IPR002035; VWF_A.
Pfam; PF01839; FG-GAP.
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C., Butterfield Y.S.N., Krzyvinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length huma
                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller L.J., Wiebe M., Springer T.A.; "Purification and alpha subunit N-terminal sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 20-43.
MEDLINE=87167596; PubMed=3549901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
              SMART; SM00191;
SMART; SM00327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send
                                               PRINTS; PR01185; INTEGRINA. PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                      PDB; 1N3Y;
                                                                                                                                                                                                                                                                                        PIR; A36584;
                                                                                                                                                                                                                                                                                                                    L; M29165; -; NOT ANNOTATED CDS.
L; M29487; AAAS1620.1; ALT_SEQ.
L; M29482; AAAS1620.1; JOINED.
L; M29483; AAAS1620.1; JOINED.
L; M29484; AAAS1620.1; JOINED.
L; M29485; AAAS1620.1; JOINED.
L; M29486; AAAS1620.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with I-domains do not undergo protease cleavage SIMILARITY: Belongs to the integrin alpha chain SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane proteinissum Specificity: Predominantly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Integrin alpha-X/beta-2 is a receptor for frecognizes the sequence G-P-R in fibrinogen. It media interaction during inflammatory responses. It is espeimportant in monocyte adhesion and chemotaxis.

SUBUNIT: Heterodimer of an alpha and a beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocytes. DOMAIN: The integrin I-domain (insert) is a VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p150,95 leukocyte adhesion [mmunol. 138:2381-2383 (1987)
                                                                                 PF01839; FG-GAP; 3.
PF00357; Integrin_alpha;
PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          M81695; AAA59180.1;
M29165; -; NOT_ANNO
                                                                                                                                                                                                                                                      N3Y; X-ray; A=141-
HGNC:6152; ITGAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement
an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acad.
                                                                                                                                                                                                                                                                                        RWHU1C
               Int_alpha; 5.
VWA; 1.
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INTEGRIN_ALPHA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
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l Similarity 24.8%;
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                                                LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 178
                                                                          NPLSLLASVHQLQ----
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                 FOALOGIIHSILKKSCIBILAABPSTICAGESFOVVVRGNGF
                                      SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND----IASKPSQEHIFKVED-
                                                                                        ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
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                                                                                                                                                                                                  326
335
1163
                                                                                                                                                                                                  AA;
                                                                                                                                                                               334
335
`*: 127886 MW;
                                                                            ; Score 143.5; DB
; Pred. No. 0.015;
43; Mismatches 8
                                                                                                                                                                                                  83658A13B5C5DE8F CRC64;
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                                                                                                                                                                             Length
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356
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Result
No.
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Maximum Match 10
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.
        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

SOURCE ORGANISM RESULT 1
AX458366
LOCUS
DEFINITION
ACCESSION
VERSION ORIGIN REFERENCE FEATURES KEYWORDS AUTHORS TITLE JOURNAL Query Match
Best Local Similarity
Matches 1104; Conserv SGS source 1414 bp Sequence 1 from Patent WO0246228 AX458366 Young, J.A., Bradley, K.A., Collier, R.: Receptor for b. Anthracis toxin Patent: WO 0246288-A 1 13-JUN-2002; WISCONSIN ALUMNI RESEARCH FOUNDATION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens AX458366.1 GI:21725038 100.0%; ilarity 100.0%; Conservative 0 /codon\_start=1
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밁 S

104

ATGGCCACGGCGAGCCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT ATGGCCACGGCGAGAGCCCTCCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT

163 60 <u>.</u>

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2 (bases 1 to 1414)
Bradley,K.A., Mogridge,J., Mous
Direct Submission
Submitted (19-SEP-2001) Departs
Wisconsin-Madison, 1400 Univer.
Location/Qualifiers
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1 (bases 1 to 1414)
Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J.
Identification of the cellular receptor for anthray
Nature 414 (6860), 225-229 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="All26496.1"
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SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKK
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AX393246  Sequence 176 from Patent WO0210217.  AX393246  AX393246.1 GI:19701296  Homo sapiens (human)  M Homo sapiens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  M Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1  St Croix, B., Kinzler, K.W. and Vogelstein, B.  Endothelial cell expression patterns  Patent: WO 0210217-A 176 07-FRB-2002;  The Johns Hopkins University (US)  Location/Qualifiers  15540	021 TGGTTCTGGCCCTCTGCTGCACTGTGATTATCAAGGAGGTCCCTCCACCCCCTGCCGAG 1	841 TGTCCAGGCCTATCTTAAAGAAGTTGGCATGAAAGTTGCAGTCCAGGTCAGGTCAGCATGAAC	1 ATCGAAATTCTAGCAGCTGAACCATCCACCATATTGTGCAGGAGAGTCATTTCAAGTTGTC	TCAGAGAGGGAGGCTATCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGCTGCTGG	CANATTCCGTCAAGGCCTAGAAGAACTCCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG CATGAAGGATTTGAAAGGGCCAGTGAGCAAGATTTATTATTATGAAAACAGACAAGGGTACAGG [
Db 804 ATCGAAATTCTGACCATCGACATGTGGACAGGTCCTCTGCAGGTTCAAG 780	541 AAAGATITCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC	504 CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAACAAGAACCAAGGGTACAGG 421 ACAGCCAGCGTCATCATTGCTTTGACTGACGAGAACTCCATGAAGATCTCTTTTTCTAT		Db 144 ATGGCCACGGAAGGCCCTCGCATCCAGCTTCCAGTGGCCTTCTTTGGCCACT 203  Qy 61 CTGGTGCTCATCTGCGCCGGAGGAGGACGCAGGAGGAGGAGGAGGAGGAGGAG	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"  ORIGIN  Query Match Best Local Similarity 99.8%; Pred. No. 0; Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Matches 1092; Tongccarccarccarcarcarcarcarcarcarcarcarcarc

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                     Receptor for b. Anthracis toxin Patent: WO 0246228-A 5 13-JUN-2002; WISCONSIN ALUMNI RESEARCH FOUNDATION
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                      Young, J.A., Bradley, K.A.,
                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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/db_xref="taxon:9606"
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AF279145
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Science 289 (5482), 1197-1202 (2000)
20407466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 5540)
St. Croix, B., Rago, C., Velculescu, V.,
Montgomery, E., Lal, A., Riggins, G.J., I
Kinzler, K.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens tumor complete cds. AF279145
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/translation="MATAERRALGIGFOWLSLATLVLICAGQGGRREDGGPACYGGFD
LUXGGGATLLEXGGYUHHWMSIYYFVBQLAHKFISPOKPGI
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SEREANRSRDIGAIVYCVGVKDFNETQLARIADSKUPVFPVNDGFQALQGIIHSLIFY
SEREANRSRDIGAIVYCVGVKDFNETQLARIADSKUPVFPVNDGFQALQGIIHSLIKK
SCIEILABEPSTICAGSSFQVVVRGNGFRHAKNVDRVLCSFKLNDSVTLANEKPSVED
TYLLCPAPILKEVGRVKAALQVSKNNGCLSFISSSVIITTTHCSDGSILAIALLILFLLL
ALALLMWFWPLCCTVIIKGVPFPPAREESEEEDDDGLFKKWFTVDASYYGGRGVGGIK
RMEVRMGEKGSTEEGGACLEKAANARVKMPEQEXFFPERALNANNARPSSFRKWYSPI
KGKLDALWALLKGYURVSVWREPGOTGRCIMFTKVKNUQPAKYPLANAYHTYSSFP
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                                                                                                                                                             /gene="TEM8"
/codon_start=1
/product="tumor endothelial
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/db_xref="GI:14017381"
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                              /gene="TEM8"
144. .1838
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                            organism="Homo
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(TEM8) mRNA,
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               TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC
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                                                                                              GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG
                                                                                                            GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG
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                                               ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGATACTTATTTACTG
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/gene="TEM8"
225..1835
/gene="TEM8"
/product="tumor 6
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Sequence 7 :
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Receptor for b. Anthracis toxin
Patent: WO 0246228-A 7 13-JUN-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (U
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX458372.1 GI:21725042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGGCCTCTCTTTATCTCCAGTTCTGTCATCATCACCACCACACACTGTTCTGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGGCCTCTCTTTTATCTCCAGTTCTGTCATCATCACCACCACACTGTTCTGACGGT
                                                                                                                                                                                                                                                    ATGGCCACGGCGAGAGCGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAGTGAGGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCATCCTGGCCATCGCCCTGCTGATCCTGTTCCTGCTCCTAGCCCTGGCTCTCCTCTGG
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                                                   GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAAATG
                                                                                                                  GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT
                                                                                                                                                                                      CTGGTGCTCATCTGCGCCGGGCAAGGGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC
                                                                                                                                                                                                                                 ATGGCCACGGCGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
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   TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA
                                  GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG
                                                                                                   GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT
                                                                                                                                                                  CTGGTGCTCATCTGCGCCCAGGCAAGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAAGA
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="unnamed protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2112 bp
from Patent WO0246228.
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                                                                                                                                                                                                                                                                                               Score 949.4; DB 6;
Pred. No. 2.6e-272;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA"
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Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schammen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Altechul, S.F., Zoeberg, B., Buetow, K.H., Schaefer, C.F.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                            BC012074 2112 bp mRNA linear PRI 29-JUN-20 Homo sapiens anthrax toxin receptor 1, transcript variant 3, mRNA (CDNA Clone MGC:19967 IMAGE:4563020), complete cds.
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           BC012074.1 GI:15082332
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                                                                                                                                                                                                                                                                                                                                      sapiens (human)
                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLIL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: g Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16933552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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Contact: MGC help desk
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                      /translation="MATAERRALGIGFOWLSLATIVLICAGQGGRREDGGPACYGGFD LYFILDKSGSVLHHWNEIYEVEQLAHKFISPQLYGGFD IVFSTRAGVIJALTEDREQIPQI RQGLEELQKVLFGGDTYMHEGFERASEQIYYENGKGFYASVIJALTDGELHEDLFFY SERBANRSRDLGAIYYCVGVKDPNETQLARIADSKOHVFPVNDGFQALQGIHGILKK SCIEILAABESTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVED TYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSLHKIASGPTTAACME"
                                                                                                                                                                                                                                                                  /product="tumor endothelial marker
/protein_id="AAH12074.1"
/db_xref="GI:15082333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonyms: FLJ10601,
/db_xref="LocusID:84168"
/db_xref="MIM:606410"
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/tissue="Kidney, renal cell
/clone lib="WIH MGC 14"
/lab_host="DH10B-R""
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/db_xref="MIM:606410"
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Best Local Similarity

86.0**%**;

Score 949.4; DB 9; Pred. No. 2.6e-272;

Length 2112;

Query Match

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RESULT 9
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St Croix,B., Kinzler,K.W. and Vogelst
Endothelial cell expression patterns
Patent: WO 0210217-A 186 07-FEB-2002;
The Johns Hopkins University (US)
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          TCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTGAAAGATTTCAATGAGACACAGCT
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                                            ATCCACCATCTGCGCGGGAGAGTCCTTTCAAGTGGTCGTAAGAGGAAATGGCTTCCGACA
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/mol_type="unassigned DN/
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Pred. No. 1.8e-243;
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//translativCyCyGYCDFMETQLARIADSKOHVFFVWDGFQALQGIIHSILKKSC
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//translativCyCyGYCMFMCGGFTASSVIITTTHCSDGSILAIALLVLFLLLAL
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Tang,Y.T., Zhou,P. and Drmanac,R.T.
Nucleic acids and polypeptides
Patent: US 6569662-A 8 27-MAY-2003;
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                             GGCGGATTTGACCTGTACTTCATTTTTGGACAAATCAGGAAGTGTGCTGCACCACCGGAAT
                                                                                                                        CTGGTGCTCATCTGCGCCCGGGCAAGGGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC
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                                                                                                        Patent: WO 0160860-A 30300 23-AUG-2001;
Millennium Predictive Medicine, Inc. (U
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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OP Primer for synthesizing full-length cDNA and use thereof.

BD156323.1 GI:27862081

BD156323.1 GI:27862081

JP 2002191363-A/11166.

Homo sapiens (human)

ISM Homo sapiens (burdata; Craniata; Vertebrata; Euteleostomi; Memanalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 1436)

Cta,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishi,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

Primer for synthesizing full-length cDNA and use thereof
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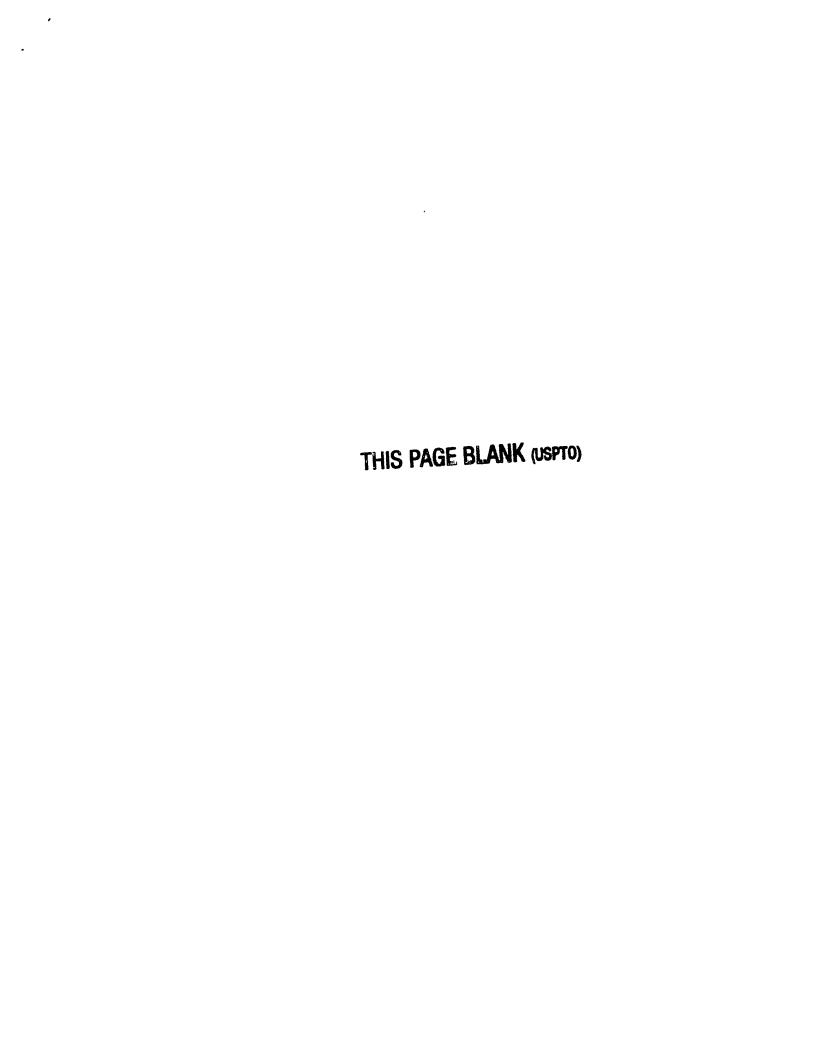
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HELIX RESEARCH INSTITUTE
OS Homo Bapiens (human)
PN JP 2002191363-A/11166
PD 09-JUL-2002
PF 28-JUL-2002
PF 28-JUL-2000 JP 2000280990
PF 28-JUL-2000 JP 2000280990
PF 28-JUL-2000 JP 2000280990
PF 3AITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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mer for synthesizing full-length cDNA and use thereof FH I
Location/Qualifiers
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KEIICHI NAGAI,TETSUJI OTSUKI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG
                                                                              TCCTTTATTGTTTTCTCCACCCGAGGAACCACCTTAATGAAACTGACAGAGAGACAGAGAA
                                                                                                                                            GAAATCTATTACTTTGTGGAACAGTTGGCCTCACAAATTCATCAGCCCCACAGTTGAGAATG
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/db_xref="GI:21725045"
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VVRGNGFRHARNVDRVLCSFKINDSVTLSKSLQSPWVSSTSGFKEGNSHPCLPARPHT
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Search completed: June 14, 2005, 15:32:17 Job time: 5150 secs



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86.0	86.0	86.0	86.1	86.1	86.3	86.3	86.3	86.3	87.0	87.0	98.7	98.8	98.8	98.8	98.8	98.8	98.8	98.8	100.0	Match	*	
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Adi00551 Human TAN	Adm64581 Human TAN	Adi00555 Human TAN	Adm64585 TANGO197	Adi00541 Human TAN	Adm64591 TANGO197	Adm64589 TANGO197	Adi00547 Human TAN	-	Adm64575 Mouse TAN	Adi00549 Human TAN	Aad05334 Human sec	Aad05303 Human sec	Adr48215 Human tum	Abx72003 DNA encod	Abx72029 DNA encod	Abv73882 Human ant	Abl92104 Human Tum	Abl92078 Human Tum	Ħ	Description		

Novel isolated polypeptide useful for identifying agent that prevents or reduces effect of anthrax toxin on host cell, for treating human or non-human animal suffering from anthrax.

Claim 7; Page 27-29; 45pp; English.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
787	787	802.2	803.8	803.8	803.8	803.8	819	853.4	853.4	853.4	853.4	867.6	867.6	892.6	912.4	912.4	949	949	949.4	949.4	949.4	949.4	949.4	949.4
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ALIGNMENTS

## RESULT 1 ABV73881 ID ABV7 CDS. WPI; 2002-713235/77. P-PSDB; ABP54903. mat\_peptide sig\_peptide 05-DEC-2000; 2000US-0251481P. 03-OCT-2001; 2001WO-US030941. WO200246228-A2 Homo sapiens. Anthrax; toxin; receptor; human; antibacterial; gene; ss. Human anthrax toxin receptor cDNA. 08-JAN-2003 (first entry) ABV73881; ABV73881 standard; cDNA; 1414 BP. Young JAT, Bradley KA, (WISC ) WISCONSIN ALUMNI RES FOUND. 13-JUN-2002. /\*tag= a /product= "anthrax toxin receptor" 104. .182 /\*tag= b 183. .1207 /\*tag= c Location/Qualifiers Collier RJ, Mogridge JS;

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11-AUG-2000;
11-APR-2001;
The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain tumour endothelial marker (TEM) protein selected from ABB90732, ABB9 ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activit:
                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                              An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                      Disclosure; Page 121-123;
                                                                                                                                                WPI; 2002-291856/33.
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11-AUG-2000;
11-APR-2001;
                        The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
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                                                                                                       TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC
                                                                                                                                       ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGATACTTATTTACTG
                                                                                                                                                    ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG
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The present sequence is that of cDNA encoding a human anthrax toxin creceptor (ATR). The cDNA, previously designated TEMB, was originally consolated by PCR from HeLa cell and human placenta cDNA libraries. It was cidentified in a database screening using a newly isolated human cDNA (see ABV73881) which encodes an ATR (see ABP54903) that is identical to the CR TEMB polypeptide except in the cytoplasmic tail, suggesting differential constitution of a primary mRNA transcript. TEMB was not previously identified constant cells, vectors, and transgenic and knock-out animals. It also constituted that the texticity of anthrax toxin. A claimed method for treating constitutes in a human or animal involves administering an agent that constitute the transcript of anthrax. Suitable agents conclude the TEMB polypeptide or a PA-binding fragment of it, a PA-binding constitute of a polygoptide at least 80% identical to these, a fusion protein, a condition and constitute or polyclonal antibody, a polyseaccharide, a lipid or a nucleic acid. ATR polynucleotides can also be used in the recombinant production
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                                     ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG
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TCCATCCTGGCCATCGCCTGCTGATCCTGTTCCTGCTCCTAGCCCTGGCTCTCCTCTGG
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                                                             The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
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Indels

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Gaps

0,

Length 5540; 0 Other;

98.8%;

Score 1090.8; Pred. No. 0;

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The present invention describes a method for detecting a pancreatic CC cancer-associated transcript in a biological sample. The method comprises CC contacting the biological sample with a polynucleotide that selectively hybridises to a sequence at least 80% identical to a sequence as shown in any one of Tables 3 to 25 in the specification or having the GenBank CC Accession Number AF279145. Also described: (1) diagnosing pancreatic CI cancer in a human or animal subject being tested, determining the CC (2) itselihood that a subject having a pancreatic cancer will survive, or CC determining the suitability of a subject having a pancreatic cancer for CC surgical resection therapy; (2) detecting a pancreatic cancer associated polypeptide in a biological sample; (3) determining the likelihood that a cc subject having a pancreatic cancer will survive; and (4) monitoring the CC efficacy of a therapeutic treatment of pancreatic activity, and can be used in CC gene and protein therapy. A pancreatic cancer associated transcript polynucleotide, a vector comprising the polynucleotide, a vector comprising the polynucleotide, an isolated comprising the polynucleotide, an isolated comprising the polynucleotide, an isolated comprising pancreatic cancer or for preparing a medicament for the treatment of pancreatic cancer or for preparing a comprising an entity of the progress of disease such cancer or its metastases, and for monitoring the progress of disease such cancer or remission or following surgery or chemotherapy. The present concerned concerned in the exemplification of the present invention.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting pancreatic cancer-associated transcript in a biological sample, useful for diagnosing or treating the disease, comprises contacting the sample with a polynucleotide that selectively hybridizes to a specific
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cytostatic; gene therapy; protein therapy;
tumour endothelial marker 8 precursor; TEM8; gene; ss.
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CC AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted CC protein genes, and AAE01436-AAE01513 represent the proteins they encode. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating CC or ameliorating medical conditions, e.g., by protein or gene therapy. CC pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in CC the new genes. Specific uses are described for each of the 28 genes, CC developing products for the diagnosis or treatment of proliferative CC developing products for the diagnosis or treatment of proliferative CC developing products for the diagnosis or treatment of proliferative CC disorders, cancer, tumours, foetal and developmental abnormalities, and include CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, allergies, schizophrenia, asthma, skin disorders (e.g., cognitive disorders, schizophrenia, asthma, skin disorders (e.g., cognitive disorders, diabetes, atherosclerosis, cardiovascular disorders,

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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrane disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                                                      New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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30-JUN-2000;
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/transl_except= (pos:688. .690, aa:Xaa)
/transl_except= (pos:1123. .1125, aa:Xaa)
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CC Pathological conditions can be diagnosed by determining the amount of the conservation of the conservation of the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, conservation of the diagnosis or treatment of proliferative conservations, foetal and developmental abnormalities, concervations, actions, altergies, concervative disorders, diseases of e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., cognitive disorders, kidney disorders, gastrointestinal disorders, cognitions also be used to aid wound healing and epithelial cell corretains can also be used to aid wound healing and epithelial cell corretains can also be used to aid wound healing and epithelial cell corretain can also be used to aid wound healing and epithelial cell corretain can also be used to aid wound healing and epithelial cell corretains can also be used to aid wound healing and epithelial cell corretains can also be used to aid wound healing and epithelial cell corretains can also be used to aid wound healing and epithelial cell corretains can be used an also be used as a food additive or corretain of the invention can be used in alleviating symptoms associated corretain of the invention can be used in alleviating symptoms associated corretain of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., readoinmunoassays or enzyme linked immunoasobent assay (ELISA). The
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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                                      inhalation anthrax; 10; ds; gene.
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                                                                                                                    fusion mutated
                                                                                                                                                                                                                                      DNA:
                                                                                                                    DNA - plasmid p0610
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig mutated fusion DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-lik domain (VWF) amino acid sequence and an amino acid sequence heterologous
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                                                         ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT
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                                               TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG
                                                                                                                          CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG
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AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC
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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.

A-like

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RESULT 11
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von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; mouse; TANGO197; immunoglobulin; Ig; fusion protein;
                                                                                                                                                                                                                                            (ROTT/)
(OKEE/)
(OZKA/)
                                                                                                                                                                            Rottman JB,
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DB; ADM64576.
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OZKAYNAK E.
HEALEY J J.
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ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG
                                                                                                                                   ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC
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99.8%;
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ATGGCCACGGCGGAGCCGGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT

Query Match Best Local Matches

Similarity

86.3%; 99.4%;

Score 952.4; Pred. No. 1.5e 0; Mismatches

B 10;

956;

Conservative

0;

Indels Length

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Sequence

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BP; 427 A; 454 C;

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                                                The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig FCR mutated fusion DNA of the invention.
                                                                                                                                                                                                                                                                                                            New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor Adomain (vWF) amino acid sequence and an amino acid sequence heterolog to the vWF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion; von Willebrand factor A-like domain; vWF; antibacterial; cutaneous; inhalation anthrax; human; TANGO 197 Ig FcR fusion; mplasmid pLKTOK127; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TANGO
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(OKEE/)
(OZKA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ROTTMAN J B.
) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI00546.
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Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or amellorating symptoms of anthrax comprises a von Willebrand factor A-like domain (VWF) amino acid sequence and an amino acid sequence heterologous to the VWF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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(OKEE/)
(OZKA/)
(HEAL/)
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cutaneous; inhalation anthrax; human; TANGO 197 Ig FCR fusion; wild-type;
plasmid pLKTOK129; ds; gene.
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OZKAYNAK E.
HEALEY J J.
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von Willebrand
vWF amino acid
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Synthetic.
                       20-DEC-2001;
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                                                                                                                                              US2003134786-A1
                                                                                                                                                                                                                                               fragment of crystallisation;
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                                                                                                                                                                                                                                                                antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous
inhalation_anthrax; human; TANGO197; immunoglobulin G; IgG;
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TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This sequence encodes a fusion protein comprising human TANGO197 extracellular region, minus the DG residues closest to the transmembrane region, and immunoglobulin G (IgG) fragment of crystallisation (Fc) with mutations L235A and G237A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (WWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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O'KEEFE T
OZKAYNAK
HEALEY J
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                     ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAAACTCCATGAAGATCTCTTTTTCTAT
                                                                                            CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG
                                                                                                                                      CAPATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG
                                                                                                                                                                      CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG
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ilarity 99.4%;
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0; Mismatches 6;
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                        ameliorating domain (vWF) to the vWF.
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                                                                                                                                                                                                                                                                                (ROTT/)
(OKEE/)
(OZKA/)
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                                        TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or liorating symptoms of anthrax comprises a von Willebrand factor A-like ain (VWF) amino acid sequence and an amino acid sequence heterologous
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DB; ADM64592.
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OZKAYNAK E.
HEALEY J J.
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                                                                       The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This sequence encodes a fusion protein comprising human TANGO197 extracellular region, minus the DC residues closest to the transmembrane region, and immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                         Example;
                                                   fragment of crystallisation (Fc).
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Sequence 1650 BP; 427 A; 453 C; 419 G; 351 T; 0 U;

0 Other;

В ş 밁 ş 5 8 문 문 S ð ફ 밁 5 ঠ δ 밁 밁 ક В S 밁 S 밁 δ 밁 밁 8 Matches Query Match Best Local 661 661 601 601 541 541 481 481 421 421 721 361 361 301 301 241 181 781 721 241 181 121 121 956; 61 61 H Similarity ATGGCCACGGCGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTTGAAGAAGTCCTGC AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTTCCC GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACCGGAAT CTGGTGCTCATCTGCGCCGGGCAAGGGGGGGACGCAGGGATGGGGGTCCAGCCTGCTAC 120 ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGC ANAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC TCAGAGAGGGGGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTTGTTTACTGTGTTGGTG ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCCATGAAGATCTCTTTTTCTAT CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGA TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT CTGGTGCTCATCTGCGCCGGGCAAGGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT Conservative 86.3%; Score 952.4; Pred. No. 1.5e 0; Mismatches <u>.</u> ; DB 11; 1.5e-281; 6; Indels Length 0 180 840 180 120 60 780 780 720 720 660 600 600 540 540 480 480 420 360 300 300 240 660 420 360 240

	Search completed: June 14, 2005, 14:06:24 Job time : 704 secs	Search completed: J Job time : 704 весв	Sear Job
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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  US-09-620-312D-8
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US-09-949-016-16291
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Sequence 8, Appli
Sequence 250, App
Sequence 297, App
Sequence 297, App
Sequence 14, Appl
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e 25,	Sequence 25, Appl	Sequence 1, Appli	Sequence 2968, Ap	Sequence 3, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli								

## ALIGNMENTS

RESULT 1 US-09-620-312D-8

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; ORGANISM: Homo sapiens FEATURE: FATURE: ; NAME/KEY: CDS ; LOCATION: (309)..(1202) US-09-620-312D-8
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APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: No. 901poptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF 580 ID NOS: 1105
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Reiyan
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Jian Rui
APPLICANT: Jian 
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Best Local Similarity
Matches 805; Conserv
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GENERAL INFORMATION:
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/ Sequence 250, Application US.
/ Patent No. 6783969

/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Zhang, Jie
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Wang, Jian-Rui
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/ APPLICANT: Mang, Yunging
/ APPLICANT: Chen, Rui-hong
/ PPLICANT: Wang, Zhiwei
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APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783959el Nucleic Ac
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 250
LENGTH: 3981
TYPB: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)..(1118)
              Sequence 297, Application US/09774528
Patent No. 6743619
Patent No. 6743619
Patent No. 6743619
PAPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Chou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
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Pred. No. 3.6e-159;
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APPLICANT: Wue, Aldong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Ac.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
FILE REFERENCE: 802
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Best Local Similarity
Matches 546; Conserv
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SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 297
LENGTH: 1492
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CURRENT FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (79)..(1434)
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; Sequence 14, Application US/082; Patent No. 5670367; GENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G.
                                                            US-08-232-463-14
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   Matches
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                          TOPOLOGY: line IMMEDIATE SOURCE: CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 91 1:
APPLICATION NUMBER: EP 91 1:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 Dia
CITY: Alexandria
                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                         TELEPHONE: (703)836-93
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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                                                                                                                                                                               LENGTH:
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                                                                                                                                                              H: 7218 base pairs
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1800 Diagonal Road
4.3%; Score 47; DB 1; Length 721 ilarity 6.7%; Pred. No. 0.00078; Conservative 199; Mismatches 164; Indels
                                                                                                                              linear
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US-08-232-463-14/c

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; ORGANISM: Homo sapiens
US-09-621-976-8976
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US-09-621-976-8976/c
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SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
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APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
INTEL OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENOST.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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                                                                        104 RYRRYWYYAKRAKWSKRCTWSTTCYCMKYMAKKCWSYWWSMSMMKWGKSMWWKWTYYYYY
                                                                                                          186 CTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATGTCCTT 245
                                                                                                                                                                                        126 ATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAATGAAAT 185
                                                                                                                                                                                                                              929 TCATCACCACCACCACGTTCTGACGGTTCCATCCTGGCCATCGCCTGCTGATCC 988
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YMMKWSKMTYWSMMSCYARKCWRTYAKTYTWMTCMTWGKR 5
                                  TATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTG 285
                                                                                                                                                  RKWTRWTYYYYKSYMSMKKTWRMKTAYYWTKRWKMTRTKWTWCTMCWKCTTYWMAGTMMY
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Alexandria
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                                                                                                                                                                                                                                                                                     263 GAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAAAAATCCGTCAAGGCCTAGAAG
                                                                                                                                                                                     TGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTC
                             CTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTGAAAGATTTCAATGAGACACAGC 562
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1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7218 base pairs
                                                                                                                                                                                                                                                                                                                                               3.8%; Score 41.4; DB 1; Length 7218; ilarity 6.8%; Pred. No. 0.055; Conservative 198; Mismatches 174; Indels 0
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PATENT NO. 6784342

GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Tran
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
PEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1
US-09-806-708B-22
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US-09-806-708B-22
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Best Local Similarity 9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                584 AGGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                               464 AAGATCTCTTTTTCTATTCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                        278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 AGACAAGGGTACAGGACAGCCAGCGTCATCATTGCTTTTGA--CTGATGGAGAACTCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 DDKRTRWWKKNNNATGWDDDTKYHMWNNNGCBTVTWMVRYKTDRDWSBKRMNYGMBWWK 217
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        TCCTCTGCAGCTTCAAGATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGG
                                             NYARABHYGYKWNTRWWBWSHTWBHBRAGAAHYWMBMMYBAKCHCMKAWYKAKKYAGAGG
                                                                                     AGTCATTTCAAGTTGTCGTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGG
                                                                                                                             WDYWWKACTWYKYBVCSKWWNNYAAWYTKSSWNYTSRYYRWKTNNSWRWRSDTRSMGRAN
                                                                                                                                                                  TTTTGAAGAAGTCCTGCATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAG
                                                                                                                                                                                                            RAWDHKTCTHNNTTWWKMKTYWNNCYWKSMTNGKSHRBAAAVYTWYMWWWRRYAHANNNN
                                                                                                                                                                                                                                                                                          VNNNNGTTMWKRMWAWYWKMDMDWBGTYNNNNNGGRTYYGWTKNKKMWTYYKWKANNCKW
                                                                                                                                                                                                                                                                                                                               TTTACTGTGTTGGTGAAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTA 583
                                                                                                                                                                                                                                                                                                                                                                       KWSAAMGVYWNNNNNWTYKKARHBARWDWVWHSAWKKWHANAAHYSRKKWTBYKRKTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGACACTTACATGCATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAAC
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9.8%; Pred. No. 0.026;
1ve 270; Mismatches
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GENERAL INFORMATION:
APPLICANT: The University of British Columbia
ITILE OF INVENTION: Regulation of Embryonic Tran
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
                                                                                                                                                                                                                         US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
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; NAME/KEY: misc_feature
; LOCATION: (1)...(37822)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-16291
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SOFTWARE: FastSEQ for
SEQ ID NO 16291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16291, Application Patent No. 6812339
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                          Similarity
                                                                                                                                                                                                 ACCCGAGGAACAACCTTAATGAAACTGACAGAGACAGAGAGAACAAATCCGTCAAGGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNNNNNNNNNNNNNNNATCARDDYYAASRWYAMANAKWYYYKBAANNAYYTHANNWWGC
TCCAGTTTTCAGCAAAACGTATAAGACACACAAAGAAACAGGAAAGTATGGCTCAT 8032
                                                                              CAAGAAACCCAGGTAGGGGAAAGAATCTGAGTTTCTAGAATAGACACATTATTTTAAATG
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Pred. No. 0.54;
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S OF DETECTION
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Transcription in Plants

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OTHER INFORMATION: consensus sequence of A.t., L.a., and
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TYPE: DNA
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                                   CCACCCCTGCCGAGGAGAGTGAGGAAAATAAAATAAAA 1104
                                                                                                          crescrerecresiesricresececererecaererearrareaaesaesrecer 1065
                                                                                                                                                   HMNTHCTYGNNTWGSAYBMAAMSMWAAGASNBVTYNWCWRMTYMGKTMTNNNNNNKAWYY
                                                                                                                                                                                                                            MRVAWMYSRDTTNTDWMWTSDWBWHWYTVDYTMMRAWNNNNNNWRBCKTTSWMWWMD
                                                                                                                                                                                                                                                                 CAGGTCAGCATGAACGATGGCCTCTCTTTATCTCCAGTTCTGTCATCATCACCACCACA
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 KCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRMAHHHW 175
                                                                          RTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWYYBMYMGKHHWBWWRRABHRSWNMWWV 214
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RESULT 10 US-08-728-323A-1/c ; Sequence 1, Application

US/08728323A

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                                                                     RESULT 11
US-09-298-568-1/c
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US-08-728-323A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
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GENERAL INFORM
APPLICANT:
APPLICANT:
APPLICANT:
Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
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Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEB: Cooper & Dunham LLP
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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Pred. No. 0.
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RESULT 12
US-09-410-399-1/c
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; TYPE: DNA
; ORGANISM: Kaposi's
US-09-410-399-1
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CORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
SEQ ID NO 1
                                                                                                                                                                                                                                    Matches
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Best Local :
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SEQ ID NO 1
LENGTH: 3489
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CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
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APPLICANT: Kaye, Kenneth M.
TITLE OP INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OP RHADINO
TITLE OP INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT EPPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-19
MUMBER OF SEQ ID NOS: 3
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                          CTCCTCGTCATCCTCGTCATCCTCCTCGTCATCCTCGTCATCCTCCTCGTCATC 1030
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llarity 50.3%;
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Pred. No. 0.67,
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Pred. No. 0.67;
0; Mismatches 91;
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; ORGANISM: Kaposi's
US-09-894-273-1
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Patent No. 5849564
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Best Local Similarity
Matches 92; Conserv
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APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
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                  ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                         APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: MOORE, POLYERPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                    STREET: 1185 Ave
CITY: New York
STATE: New York
COUNTRY: U.S.A.
COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1029
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1185 Avenue of the Americas
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Conservative
IBM PC compatible
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Pred. No. 0.67;
0; Mismatches 91;
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RESULT 15
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Best Local Similarity
Matches 92; Conserv
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APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Ro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNAY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: MOORE, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/757,669A
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        FILING DATE:
                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                             CITY: New York
STATE: New York
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TOPOLOGY: linear
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1185 Avenue of the Americas
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Pred. No. 3.5;
O; Mismatches
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; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic US-08-757-669A-20
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Matches 92; Conserv
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TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                   20968 CTCCTCGTCCTCATCTGTCTCCTGCTCCTCATCATCCTTATTGTCATTGTCATC 21027
                                                                                                                                      20908 CTCCTCGTCATCCTCGTCATCCTCCTCGTCATCCTCGTCATCCTCCTCGTCATC 20967
21028
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CTT 21030
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                                                                                                                                                                                                       CTCCTCGTCATCCTCGTCATCCTCCTCGTCATCCTCCTCGTCATCCTCCTCGTCATC
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Search completed: June 14, 2005, 16:47:10 Job time: 233 secs

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Maximum I
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Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
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/ Cgn2_6/ptodata//pubpna/USOB_NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/USOP_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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US-10-133-937-58 US-10-159-563-58 US-09-918-715-176 US-09-918-715-31 US-09-918-715-31 US-10-301-822-198 US-10-474-794-176 US-10-474-794-231	ID
Sequence 58, Appl Sequence 58, Appl Sequence 176, App Sequence 231, App Sequence 198, App Sequence 176, App Sequence 231, App	Description

## ALIGNMENTS

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                                                                                                                                                                     ; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
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Publication No. US20030207278A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
TITLE OF INVENTION: OTHER BIOLOGICAL STATES
FILE REFERENCE: 11613 56USO1
CURRENT APPLICATION NUMBER: US/10/133,937
CURRENT FILING DATE: 2002-11-04
144 ATGGCCACGGCGGAGCGGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 203
                      1 ATGGCCACGGCGGAGAGCCCTCGGCATCCAGTGGCTCTCTTTGGCCACT
                                                                                                 100.0%; Score 1104;
100.0%; Pred. No. 0;
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                                                           TGGTTCTGGCCCCTCTGCTGCACTGTGATTATCAAGGAGGTCCCTCCACCCCCTGCCGAG
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US-10-159-563-58

US-10-159-563-58

Sequence 58, Application US/10159563

Publication No. US2004009154A1

GENERAL INFORMATION:

APPLICANT: Khan, Javed

APPLICANT: Khan, Javed

APPLICANT: Ringner, Markus

APPLICANT: Meltzer, Paul

TITLE OF INVENTION: SELECTIONS OF GENES AND

TITLE OF INVENTION: DIAGNOSIS AND FOR TARGE

FILE REFERENCE: 11613-56US11

CURRENT APPLICATION NUMBER: US/10/159,563

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: US 10/133,937

PRIOR APPLICATION NOMBER: US 10/133,937

PRIOR APPLICANT: APPLI
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1104; Conservative 0; Mismatches
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RESULT 4
US-09-918-715-231
; Sequence 231, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
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APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAI
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOSTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 231
LENGTH: 5540
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                                                     ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC
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Pred. No. 0;
0; Mismatches
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APPLICANT: TIABOGEAU, Stephen N.

APPLICANT: BUEGATT, LAWTENCE J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE

TITLE OF INVENTION: THERAPY OF COLON CANCER

FILE REFERENCE: MEMO1-029P2RNM

CURRENT APPLICATION NUMBER: US/10/301,822

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR FILING DATE: 2001-12-10

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR APPLICATION NUMBER: US 60/361,988

PRIOR APPLICATION NUMBER: US 60/361,988

PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

SOFTWARE: F8stSEQ for Windows Version 4.0

SEQ ID NO 198

LENGTH: 5540
                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LCCATION: (144)...(1838)
US-10-301-822-198
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Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
                                                                                                                           Query Match
Best Local Similarity
                                                                                                              Matches 1092;
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APPLICANT:
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                                                            ATGGCCACGGCGAGAGCGCAGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
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   CTGGTGCTCATCTGCGCCCGGGCAAGGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC
                                       ATGGCCACGGCGGAGCCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
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Schlegel, Robert
Monahan, John E.
                                                                                                              Conservative
                                                                                                                           98.88;
                                                                                                            Score 1090.8;
Pred. No. 0;
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APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT FILING DATE: 2003-10-14
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FASTSEQ for Windows Version 4.0
ENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
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Matches 1092; Conserv
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Publication No. US20040213793A1
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                                                                   GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGC
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APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Vincer, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATELLE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 50/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOPTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 231
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-474-794-231
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US-10-474-794-231
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                                                                                                                                                                                                Local Similarity
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Pred. No. 0;
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                                                                                     US-10-038-307-17
                                                                                                   RESULT 8
Sequence 17, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
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APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1674
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-17
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                                                 GTGAGAGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG
                                                                                                  ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC
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ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGATACTTATTTACTG
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Pred. No. 3.9e-303;
0; Mismatches 2;
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Sequence 17, Application US/10201292

Sequence 17, Application VS/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEBFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and FILE REFERENCE: 7953-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT PILING DATE: 2003-02-14

INUMBER OF SEO ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 1674

TYPE: DNA

ORGANISM: Homo sapiens
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             TCAGAGAGGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTTGTTTACTGTGTTGGTGTG
                                                                                                                       CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG
                                                                                                                                                                  CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGGAGACACTTACATG
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                                                  ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT
                                                                                                   CATGAAGGATTTGAAAAGGGCCAGTGAGCAGATTTATTATGAAAAACAGACAAGGGTACAGG
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99.8%;
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Pred. No. 3.9e-303;
0; Mismatches 2;
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300

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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1650
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-13
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Best Local S
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99.4%;
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Pred. No. 2.2e-300;
0; Mismatches 6;
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 GENERAL INFORMATION:

APPLICANT: James B. ROTTWAN

APPLICANT: Engin OZKAYNAK

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Cor

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FASTSEQ for Windows Version 4.0

SEG ID NO 15

LENGTH: 1650

TYPE: DNA
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Publication No. US20030134786A1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-13
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US-10-201-292-13
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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Best Local Similarity 99.4%;
Matches 956; Conservative
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Pred. No. 2.2e-300;
0; Mismatches 6;
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Sequence 15, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-99
CCURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-15
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Pred. No. 2.2e-300;
0; Mismatches 6;
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US-10-038-307-9
; Sequence 9, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-9
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Best Local Similarity
Matches 955; Conserv
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                                                                                                                                                                                           APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
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                                                                  86.1%;
                                                       Score 950.8; DB 15
Pred. No. 7.3e-300;
0; Mismatches 7;
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RESULT 15
US-10-201-292-9
US-10-201-292-9
Sequence 9, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
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; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-9
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Search Job tin	문	Ş	당	Ş	망	Ş
Search completed: June 14, 2005, 18:37:32 Job time : 786 secs	961 TC 962	961 TC 962	901 GATGGCCTCTCTTTTATCTCCAGTTCTGTCATCACCACCACACACTCTTCTCCCAAA 960	901 GATGGCCTCTTTTATCTCCAGTTCTGTCATCATCACCACCACACACA	841 TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 900	841 TGTCCAGCGCCTATCTTAAAAGAAGTTCGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 900

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Result
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                  1 ATGGCCACGGGGGGGGGGGGGCCTCCGGCATCGGCTTCCAGTGGCCTCTCTTTGGCCACT
                                                                                                                                                                                                                                                                                           division of Invitrogen.
Location/Qualifiers
1. .1957
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JUL-2004) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pull-length cDNA libraries and normalization Unpublished Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1957)
1 (bases 1 to 1957)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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HTC; CNSLT_cDNA.
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO35YA13"
/tissue_type="Placenta Cot 2"
/plasmid="pCMVSPORT_6"
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AK031465

MIS MISCULUS 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030436P19 product:ANTRAX TOXIN RECEPTOR PRECURSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], fu
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18 (bases 1 to 3161)

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19 Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, M., Hiramoto, K., Kanaka, I., Kasukawa, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Sahto, H., Sakai, C., Sakai, K., Sakacume, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission

10 Direct Submission

11 Submission
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                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on
of 60,770 full-length cDNAs
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Eukaryota; Metazoa;
                                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenant Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
                                                     URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
                                                                                                                         prepare mouse tissues.
Please visit our web site for
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MARKER 8) homolog [Mus musculus] (SWISSPROT|Q9CZ52,
evidence: FASTY, 100%ID, 84.6%length, match=1428)"
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5-PRIME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence belongs to sequence cluster 1660.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODEO11CF05QP1&c=1660.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was not normalized. Library was constructed by Life Technologies, division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 9157 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web 1: www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr voligo(dT) primer. Five prime
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced Contact: Genoscope
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1 (bases 1 to 106)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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  CTGGTGCTCATCTGCGCCCGGGCAAGGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC
                                        ATGGCCACGGCGGAGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
                                                                   ATGGCCACGGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
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Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YL09
mRNA sequence.
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/clone="Vector: pc/WySPORT 6; lst strand cDNA was primed
/note="Vector: pc/WySPORT 6; lst strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pc/WYSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                          clone="CS0DE011YL09"
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99.0%;
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Pred. No. 4.3e-193;
1; Mismatches 4;
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11448 row: n column: 07
                                                                                                                                                                1 (bases 1 to 878)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                              BI823853
603039031F1 NIH_MGC_115 Homo
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                           mRNA sequence.
BI823853
                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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                    quality sequence stop: {
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/organism="Homo sapiens"
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/lab host="NH1_MGC_T15"
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/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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1 ATGGCCACGGCGGAGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTTGGCCACT Similarity CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGGAGACACTTACATG GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT CTGGTGCTCATCTGCGCCCGGGCAAGGGGAGGGAGGATGGGGGGTCCAGCCTGCTAC GTCGTGAGAGG---AAACGGCTTCCGACATGCCCG--CAACGTGGACAGGG---TCCTCTG CATC-GAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTC-ATTTCAAGTT GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTTG-AAGAAGTCCTG AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTTCCC ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCCATGAAGATCTCTTTTTCTAT TCCTTTATTGTTTTCTCCACCCGAGGAACCACCTTAATGAAACTGACAGAAGACAGAGAA GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG GGCGGATTTGACCTGTACTTCATTTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT CTGGTGCTCATCTGCGCCGGGCAAGGGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC ATGGCCACGGCGGAGCGGAGAGCCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT CATCGGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCAATTCCAAGTT GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAAGAAGTCCTG TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCCATGAAGATCTCTTTTTCTAT CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA Conservative 62.0**%**; 95.1**%**; <u>,</u> Score Pred. Mismatches e 684.6; DB 4; . No. 9.4e-192; ismatches 29; Indels Length 878; 11; Gaps 655 600 595 540 536 480 476 420 416 360 356 296 236 180 176 9 775 715

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                                               L. Nature 420, 563-573 (2002)

E 6 (Dases 1 to 1614)

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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Adachi, J., Alzawa, K., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, N., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, H., Iroh, M., Izawa, M., Kishi, Y., Konno, H., Kouda, M., Kouda, T., Kouda, M., Kojima, Y., Konno, H., Kouda, M., Kishi, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   936
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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1614 bp mENA linear HTC 03-APR-2004
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810405N18 product:ANTRAX TOXIN RECEPTOR
PRECUNSOR (TUMOR ENDOTHELIAL MARKER 8) homolog [Mus musculus], full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GARAGARAGATCCAARAGCTCTTTTTTTTTTTTTTTTVN 3,], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rot = 37.5. Second strand cDNA was of sequence [5'
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                                                                                                                 ACAACCTTAATGAAACTGACAGAAGACACAGAGAATCCGTCAAGGCCTAGAAGAACTC 327
CAGAAAGTTCTGCCAGGAGAGACACTTACATGCACGAAGGATTCGAGAGGGCCAGTGAG 121
                                                                                                                                                                                                                       CAGAAAGTTCTGCCAGGAGGAGACACTTACATGCATGAAGGATTTGAAAGGGCCAGTGAG 387
                                                                                                                                                                                                                                                                                                 ACAACTTTAATGAAACTAACTGAGGACAGGGAACAGATCCGACAAGGCCTAGAAGAGCTC 61
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GLPKKKWPTVDASYYGGRGVGGIKRWEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYE
FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTRFRGWR
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GGYRFASVIIALTDGELHEDLFFYSEREANRSEDLGAIVYCVGYKDFNEFQLARIADS
KDHYFPVNDGFQALGGIIHSILKKSCIEILABAPSTICAGESFQVVVRGNGFRHARNS
KDHYFPVNDGFQALGGIIHSILKFYSERARESFTCAGESFQVVVRGNGFRHARND
DRVLCSFKINDSVTLNEKPFAVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSV
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/protein_id="BAB28591.1"
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
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                                        Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12238 row: j column: 13
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1054)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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AGENCOURT 6420797 NIH MGC 72
5', mRNA Bequence.
BM800898
                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
  /organism="Homo
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/db_xref="taxon:9606"
/clone="IMAGE:5541228"
/tissue_type="melanotic melanoma"
/lab_hoEt="DH10B (phage-resistant)"
/clone lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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0; Mismatches 15;
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High quality sequence start: 6
High quality sequence stop: 688.
Location/Qualifiers
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C0245219
C0245219.1 GI:49108057
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Tissue Procurement: Mary Hendrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 833)
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Homo sapiens
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                                                                                                                                           GAAATCTATTACTTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG 240
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                                                                                                               GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG
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                       TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:30924322"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab host="DH108 (T1 phage resistant)"
/clone lib="NH MGC 212"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at: image.l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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              /note=Torgan: ovary; Vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. DIrectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3948114"
                                                                                                                                                                                                                                   /tissue_type="adenocarcinoma cell line"
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/clone_lib="NIH_MGC_9"
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                                                                                                                                                                                   mRNA sequence.
BG326444
BG326444.1 GI:13132881
              Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov
                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                      Homo sapiens (human)
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                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                          Catarrhini;
                                                             Mammalian
                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                    cDNA clone IMAGE: 4563020 5',
                                                           Gene Collection (MGC)
                                                                                                          Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                  CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGGAGACACTTACATG
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GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCACTCAATT
                                                                                                                            TCAGAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGTTG
                                                                                                                                                                                                     ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT
                                                                                                                                                                                                                                      CATGAAGGATTCGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG
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                                              AAAAGATCTCATGAGACAAGTTTGGCC--GGATGCGGACAGTAAGGATCATGTGTATCCC
                                                                    AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTTCCC
                                                                                                                                                                        ACAGCCAGCGTCATTGATTGACTGATGAGAACTCCATGAAGATCTCTTTTTCTAT
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Location/Qualifiers
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/tlssue_type="renal cell adenocarcinoma"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 14"
/clone lib="NIH MGC 14"
/note="Organ: kldney; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by Oligo-dT priming. Directionally
Cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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96.3%;
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Pred. No. 4.2e-162;
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammalian
Unpublished (1999)
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BG281561
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
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                                                             GTCCT--TTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGA 297
                                                                                                                                                                                                           GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT 180
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GAACAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTAC 357
                                                                                                              GAAATCTATTACTTTGTGGAACAGTTGGGTTCACAATTTCATCAGCCCACAGTTGAAAAT
                                                                                                                                               GAAATCTATTACTTTGTGGAACAGTT-GGCTCACAAATTCATCAGCCCACAGTTGAGAAT 239
                                                                                                                                                                                                                                                                                                                                           ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4544691"
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/lab_host="BH10B (phage-resistant)"
/clone lib="NIH MGC 20"
/clone lib="NIH MGC 20"
/clone lib="NIH MGC 20"
/clone dib="NIH MGC 20"
/clone dinto EcoRI/XhoI sitee using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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96.1%;
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Pred. No. 2e-161;
0; Mismatches 19;
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CF132432.1
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UI-HF-FQ0-awo-m-16-0-UI.r1 NIH_MGC_215
IMAGE:30560079 5', mRNA seguence.
                                                                                                                                                                                                                                                                                                                                                                   375 Newton Road , 4156 MEBRF, Iowa City, Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Mary Hendrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                Coordinated Laboratory
University of Iowa
375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact:
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97044477
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Bonaldo, M.F., Lenno
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two appr
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Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of cDNA Library Arrayed by: Dr. M. Bento Soares, University of DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
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375 Newton Road , 4156 MEBRF, Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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/lab host="PH108 (TI phage resistant)"
/clone_lib="NH108 (Ti phage resistant)
/clone_lib="NH108 (Ti phage res
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Pred. No. 3.6e-149;
0; Mismatches 1;
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
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TTGGACAAATCAGGAAGTGTGCTGCACCACTGGAATGAAATCTATTACTTTGTGGAACAG
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1: 01612008930
x: 01612360409
                                                                                                                                                                                                                                                                                                                                                  /notes Torgan: trunks; Vector: pBluescript II KS(+);
/notes Torgan: trunks; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: Not1; Modification of pBluescript
II KS(+) [Stratagene] vector to accommodate cDNA produced
with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
containing BsgI and BamHI sites
[5'ggccgcgtgcagcccggatccggaaaaaaaag]
[5'aattcttttttcggatccggagccgcacgc]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="White Leghorn,
/db_xref="taxon:9031"
/clone="ChEST73e23"
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/lab_host="DH10B"
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                                                                                                                                       Unpublished (2003)
Contact: Speleman, F.
Center for Medical Genetics
                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Butheria; Primates; Catarrhini; Hominidae; 1 (base 1 to 564)
De Preter, K., Pattyn, F., Berx, G., Menten, B., Van Roy, Paepe, A., Speleman, F. and Vandesompele, J.
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g2b4 IMR32_SSH Homo mapiens
CD664532
                                             Tel: 3292402451
Fax: 3292404970
                                                                                       Ghent University Hospital
De Pintelaan 185, 1K5, 9000 Ghent,
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                      franki.speleman@UGent.be
  Location/Qualifiers
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                                                                                          Belgium
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---- 545; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hc
1 (bases 1 to 877)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ
                                                                                                                         877 bp mRNA linear EST 08-APR
EX364961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens
clone CSODIO35YAl3 5-PRIME, mRNA seguence
                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                       Homo sapiens
                                                                                                          BX364961.2 GI:46288818
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                                                                                  sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/cell type="Neuroblastoma"
/cell line="IMR-32"
/lab host="Seherichia coli"
/clone lib="IMR32 SSH"
/note="Vector: pGEM-T Basy; PCR select - su
subtractive hybridisation (SSH)"
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96.6%;
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Pred. No. 7.7e-147;
0; Mismatches 18;
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                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr
Email: segref@genoscope.cns.fr
Email: segref@genoscope.cns.fr
Int strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS1AI009ZE07QP1&c=1660.f. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATGTCCTTTATTGTTTTCTCCACC
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                                                                                                    GCTGGCCCGGATTGCGGACAGTTAGGRTCATGTGKKKCSCGTGAATSACGGCTTTCAMGC
                                                                                                                                            GCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGC
                                                                                                                                                                                                                                          TCTCGAGATCTTGGTGCAATTGTTTACTGTGTT-GGTGTGAAAGATTTCAATGAGACACA
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                            TCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCCTGCATC
                                                                                                                                                                                                                TCTCSAGATCTTGGTGCAAWTRTTTACTGTGTTKGGTGTKAAAGATTTCAATGAGACACA
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/db_xref="taxon:9606"
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Pred. No. 3.6e-146;
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Job time : 4263 secs



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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Maximum Match 100%
Listing first 45 summaries
                           GQGGRREDGGPACYGGFDLY.....GLSFISSSVIITTTHCSDGS
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                         US-08-362-652-46
US-08-605-672-46
US-08-943-333-46
US-09-193-043-46
US-09-193-043-46
US-09-188-307A-46
US-09-188-307A-46
US-09-188-307A-46
US-09-188-307A-53
US-08-605-672-53
US-08-943-635-53
US-09-193-043-53
US-09-193-043-53
US-09-193-043-53
US-08-485-618-37
US-08-485-618-37
US-08-485-618-37
US-08-362-652-37
US-08-362-652-37
US-08-943-253-37
US-08-943-253-37
US-08-943-253-37
US-08-943-253-37
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US-08-362-652-46
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## ALIGNMENTS

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                                            Query Match
Best Local Similarity 28.2
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
PILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 238,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 51
                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                LENGTH:
11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicago
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                             312-474-0448
                                                         10.8%; Score 166; DB 1; I
28.2%; Pred. No. 6.9e-09;
vative 42; Mismatches 96;
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US-08-485-618-46
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US-08-485-618-46
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                                                                                 Matches
                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                       TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPUTER: TOWN PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485,61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 5-AUG-1994
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                        LENGTH: 1155
TYPE: amino acid
TYPE: 11near
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                                  11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
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  PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                 Conservative
                                                                                                                                                                                   protein
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                                                                            10.8%; Score 166; DB 1; Length 1155;
28.2%; Pred. No. 6.9e-09;
Live 42; Mismatches 96; Indels 3
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US-08-362-652-46
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                                                                                                                                                                                         Matches
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GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1155 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 25-3856
                                                                                                                                                                                       / Match 10.8%;
Local Similarity 28.2%;
nes 66; Conservative 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
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                                                                                                              144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                   204 FTEFKSSLSPQSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
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                                                                                                                                                 11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK
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                                                                                                                                                                                                                                                                                                         amino acid
XGY: linear
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TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                        LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                          1155 amino acids
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                                                                                                                                                                                         Score 166; DB 1;
Pred. No. 6.9e-09;
2; Mismatches 96
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US-08-605-672-46
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US-08-605-672-46
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
PILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acid
TYPE: amino acid
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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CITY: Chicago
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                               123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
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                                                                     204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
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                                                                                                                                                               11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
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                                                                                                     LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
                                                                                                                                           PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                                                                                                                                                                                                                                                                                         TYPE:
TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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                                                                                                                                                                                                                10.8%; Score 166; DB 2; I
28.2%; Pred. No. 6.9e-09;
tive 42; Mismatches 96;
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,6
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORWATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
APPLICATION NUMBER: US 08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
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PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                         TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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                                                                                  TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
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Pred. No. 6.9e-09;
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
PILING DATE: 23-DEC-1993
PRICE 23-DEC-1993
PRICE SAUGHT S
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Gallatin, W. MICHAEL
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha
TITLE OF INVENTION: 114
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 1155 amino acids
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316
                                                            174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                  259
                                                                                                                                                                                                  123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                                                                                                     204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                        144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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233 South Wacker Drive, 6300 Sear Tower
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IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
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US-09-688-307A-46
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                                          PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-12-21
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SEQ ID NO 46
LENGTH: 1155
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Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
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Best Local Similarity
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EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
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CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
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EARLIER FILING DATE: 1994-08-05
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                                        APPLICATION NUMBER: 08/286,889
FILING DATE: 1994-08-05
APPLICATION NUMBER: 08/362,652
FILING DATE: 1994-12-21
APPLICATION NUMBER: 08/943,363 FILING DATE: 1997-10-03
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; ORGANISM: Mus musculus
US-09-350-259-46
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US-09-350-259-46
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SEQ ID NO 46
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Best Local (
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
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CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6620915el Human
FILE REFERENCE: 27866/35004
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EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
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EARLIER APPLICATION NUMBER: 08/173,497
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TYPE: PRT
ORGANISM: Mus musculus
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                                                                                 204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
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                                         TDGELHEDLFFYSB--REANRSRDLGAIVYCVGVKD-FNB-TQLARI-----ADSKDHVF 173
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TDGOKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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Pred. No. 6.9e-09;
42; Mismatches 96; Indels 3
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Pred. No. 6.9e-09;
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Best Local Similarity
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

PILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 1161 amino ac
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 572853361 Human
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APPLICATION NUMBER: US 08/173,497
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 233 Street Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                        259
                                                                                                                       204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
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o. 572853
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                                                                                                                                                           69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
                                                                                                                                                                                                                                                                                    66;
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PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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                                      TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                              TDGBLHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                                   PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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Pred. No. 6.9e-09;
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RESULT 11
US-08-362-652-53
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-362-652-53
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Best Local (
                                                                                                                                                                                                                                                                                                       Matches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE THAT Amino aci
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FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELEFAX: 312-474-0448
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316
                                 174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVVRGNGFRHARNVD 227
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                                                                                                              123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                 204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                            144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                     69 LTEDR-----EQIROGLEELOKVLPGGDTYMHEGFERASEQIYYENROGYRTA-SVIIAL 122
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KVGN-FVALRSIORQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
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233 South Wacker Drive, 6300 Sear Tower
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Pred. No. 6.9e-09;
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                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1161;
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 364
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RESULT 12

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RESULT 13
US-08-482-293A-53
· Sequence 53, Application US/08482293A
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ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION UMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
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LENGTH: 1161 amino aci
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                    316
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                                                                                                                                                                                                                                                                                        204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                      144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                             69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL
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GY: linear
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                                                                                                                                                                                                               TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 166; DB 2; 28.2%; Pred. No. 6.9e-09; tive 42; Mismatches 96
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RESULT 14
US-08-943-363-53
J Sequence 53, Application US/08943363
J Patent No. 5837478
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US-08-482-293A-53
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Best Local Similarity
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GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
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APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human
TOTTE OF INVENTION: 103
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LENGTH: 1161 amino acids
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ATTORNEY/AGENT INFORMATION:
ANAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 233 Sc
CITY: Chicago
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                                                                                                                                                                                                                                                                             204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                       144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
CANT: Gallatin,
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                                                                                                                                                                                                  TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                                                                                                                                                                                                                                                                LTEDR-----BQIRQGLEELQKVLPGGDTYMHEGFERASBQIYYENRQGYRTA-SVIIAL
                                                                                                                            KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD
                                                                                                                                                                                                                                      TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
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PC-DOS/MS-DOS
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RESULT 15
US-09-193-043-53
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Sequence 53, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/173,497
PILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                          TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                                                                                      TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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Pred. No. 6.9e-09;
2; Mismatches 96;
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FILE REPERNCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT APPLICATION NUMBER: 09/173,497
EARLIER REPILING DATE: 1998-11-16
EARLIER REPILING DATE: 1999-12-23
EARLIER FILING DATE: 1999-12-23
EARLIER FILING DATE: 1994-00-05
EARLIER FILING DATE: 1994-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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DB seq length: 2000000000
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1536
1 GQGGRREDGGPACYGGPDLY.....GLSFISSSVIITTTHCSDGS 295
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA: *
/ cgn2_6/ptodata/1/pubpaa/US08_RUM_PUB_pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB_pep:*
/ cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB_pep:*
/ cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB_pep:*
/ cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB_pep:*
/ cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB_pep:*
/ cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB_pep:*
/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB_pep:*
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                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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153 153 153 153 153 153 153 153 153 153	Score
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US-09-833-245-621 US-09-918-715-187 US-09-918-715-232 US-10-301-822-199 US-10-408-765A-1823 US-10-474-794-187 US-10-474-794-232 US-10-474-794-232 US-10-038-307-18 US-10-038-307-18 US-10-201-92-18 US-09-833-245-620 US-09-833-245-620 US-09-796-753-12	SUMMARIES
Sequence 621, App Sequence 187, App Sequence 192, App Sequence 193, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 620, App Sequence 12, Appl	Description

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	-10-368-087-16	-10-201-	-10-038-307-	-09-796-753-	-10-047-	US-10-201-292-30	-10-201-292-	-10-201-292-	2-3	92-	US-10-201-292-12	-10-038-307-	US-10-201-292-10	-307-	լ	US-10-201-292-14		-10-038-307-	- 1	2		US-10-038-307-26	-10-474-794-3	-10-474-794-	L	-91		2		US-10-038-307-24	1-292-	US-10-038-307-2
e 2639, A 312, App	e 16,	9	е 6,	e 52,	e 99,	e 30,	ø	e 32,	34,	36,	12,	Ø	e 10,	Ø	e 16,	е 14,	e 16,	14,	e 22,	e 22,	e 26,	e 26,	e 301,	e 194,	e 301,	e 194,	e 20,	e 20,	Sequence 24, Appl	e 24,	Sequence 2, Appli	Sequence 2, Appli

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT PILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-2
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; ORGANISM: Homo mapiens
US-09-833-245-621
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                             295;
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TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                                                                                            GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
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Pred. No. 7.4e-149;
0; Mismatches 0;
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APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHBLIAL CELL EXPRESSION PA:
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                        US-09-918-715-232
                                                                                                         RESULT 3
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US-09-918-715-187
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Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
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LENGTH: 564
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Best Local Similarity
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ORGANISM: Homo sapiens
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Pred. No. 1.2e-148;
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APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS TITLE OF INVENTION: THEXAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2002-11-21
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR PILLING DATE: 2002-03-05
PRIOR FILLING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
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PRIOR FILING DATE: 2000-08-02
PRIOR PLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 232
LENGTH: 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 199, Application US/10301822 Publication No. US20030148410A1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L.
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TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
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CURRENT FILING DATE: 2001-08-01
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Pred. No. 1.2e-148;
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GENERAL AND GENERAL SOUTHERS.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Fahy, Eoin D.

APPLICANT: Tanng, Bing
APPLICANT: Gibson, Bradford W.

APPLICANT: Gibson, Bradford W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

FILE REFERENCE: 660088 465

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1823

LENGTH: 564

TYPE: PRT

GORGANISM: Homo sapiens

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US-10-408-765A-1823
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/ ORGANISM: Homo Sapiens
US-10-301-822-199
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Best Local
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Similarity 100.0%; Pred. No. 1.2e-148;
95; Conservative 0; Mismatches 0;
                   ALQGIIHSILKKSCIEILAABPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240
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o. US20040101874A1
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; ORGANISM: Homo sapiens
US-10-474-794-187
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Sequence 232, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
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SOFTWARE: RastSEQ for Windows Version
SEQ ID NO 187
LENGTH: 564
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PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
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CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
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APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
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5. US20040213793A1
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Pred. No. 1.2e-148;
; Mismatches 0;
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FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: US/10/474,794

CURRENT FILING DATE: 2003-10-14

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 60/308,829

PRIOR FILING DATE: 2001-08-01

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; ORGANISM: Homo sapiens
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18
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US-10-038-307-18
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Best Local S
Matches 294
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Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICANON NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
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SOFTWARE: PastSEQ for Windows Version 4.0
SQ ID NO 18
SQ ID NO 18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 232
LENGTH: 564
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LENGTH: 4 TYPE: PRT

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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OXAXNAK

APPLICANT: Judith J. HEALEY

ITITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 551

TYPE: PRT

ORGANISM: Homo sapiens
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
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US-09-833-245-620
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US-10-201-292-18
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                                                                                                                                                                                                                                                                                        Sequence 620, Application No. US200 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                 FILE REFERENCE: PF546PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10201292
No. US20030144193A1
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100.0%; Pred. No. 3e-148;
tive 0; Mismatches 0
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APPLICANT: MCCARTHY, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT APPLICATION NUMBER: 09/183,175
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-03-26
PRIOR PRIOR PRICING DATE: 1999-03-01
PRIOR PRICING DATE: 1999-03-04
PRIOR PRILING DATE: 1999-03-04
PRIOR PRILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR PRILING DATE: 1999-06-18
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, NAME/KEY: SITE
; LOCATION: (358)
; OTHER INFORMATION: Xaa
US-09-833-245-620
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NAME/KEY: SITE
LOCATION: (320)
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NAME/KEY: SITE
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                            FILING DATE:
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                               09/365,164
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Pred. No. 1.3e-147;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   any
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; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo s
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R FILING DATE: 2000-0;
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FILING DATE: 2000-03-01
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RESULT 12
US-10-038-307-2
(Sequence 2, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: LO'KEEFE
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions
; FILE REFERENCE: 7853-253-999
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-2
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US-10-201-292-2
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APPLICANT: Therest L. O'KEEPE
APPLICANT: Therest L. O'KEEPE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
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CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
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Publication No. US20030144193A1
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Pred. No. 2.5e-147;
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-24
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                                                                                      Sequence 24, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-99

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36
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                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 345
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Best Local Similarity
ORGANISM: Homo
                TYPE: PRT
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No. US20030134786A1
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Search com	₿ <i>&amp;</i>	B 8	B 8	B 8	B &	Query Match Best Local Matches 29	US-10-201-292-24
Search completed: June 13, 2005, 20:36:49 Job time : 96.5881 secs	241 LNEKPPSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCS 292 	181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240 	121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCYGVKDFNETQLARIADSKDHVFFVNDGFQ 180 	61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120 	1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSPIVFS 60 	Query Match 99.0%; Score 1520; DB 14; Length 345; Best Local Similarity 100.0%; Pred. No. 2.6e-147; Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	292-24

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## SUMMARIES

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92	92.5	93	94	94.5	95.5	95.5	95.5	96	96	96.5	97	97.5	98	98	98.5
6.0	6.0	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.2	6.3	6.3	6.3	6.4	6.4	6.4
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transposase (04) B	probable chaperone	hypothetical prote	undulin 1 - human	integrin alpha-1 c	integrin alpha-E c	inter-alpha-inhibi	transcription regu	probable retroelem	integrin alpha-1 -	hypothetical prote	collagen alpha 3(V	dnaK protein NMB05	collagen alpha 3(V	hypothetical prote	hypothetical prote

## ALIGNMENTS

	RESOLT: L
	RWHU1B
	cell surface glycoprotein CD11b precursor [validated] - human
	N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
	eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
	C; Species: Homo sapiens (man)
	C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
	C;Accession: A31108; A28915; Ā41600; A30892; A32218; A46526; A26091; I52567
	R; Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
	J. Biol. Chem. 263, 12403-12411, 1988
	A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CDI
	, w
	A;Reference number: A31108; MUID:88315033; PMID:2457584
	A;Accession: A31108
ted by chance to have a	A; Molecule type: mRNA
of the result being printed,	A;Residues: 1-1153 <cor></cor>
core distribution.	A;Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148

ID:g307148

A;Note: part of this sequence was confirmed by protein sequencing R;Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, Pierce, M.W.; Tenen, D.G.
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mc A;Reference number: A28915; MUID:88257215; PMID:2454931
A;Accession: A28915

A; Molecule type: mRNA
A; Residues: 1-499,501-965,'P',967-1153 < ARN>
A; Residues: 1-499,501-965,'P',967-1153 < ARN>
A; Residues: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594:
A; Note: the authors translated the codon TAC for residue 1129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was confirm R; Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regular, Reference number: A41600; MUID:92073318; PMID:1683702

A; Molecule type: DNA A; Residues: 1-9 < SHE>

A;Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215 R;Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, I Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988 A;Title: Molecular cloning of the alpha-subunit of human and guinea pig l A;Reference number: A94193; MUID:88190151; PMID:2833753

D.G.

guinea pig leukocyte adhesic

A;Accession: A30892

A; Molecule type: mRNA A; Residues: 917-1042 < AR2>

A;Cross-references: GB.M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218 receptor

A; Molecule type: mRNA A; Residues: 9-1153 <HIC>

A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home C;Reywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F;17-1108/Domain: extracellular #status predicted <EXT>
F;148-318/Domain: extracellular #status predicted <EXT>
F;1465-473/Region: calcium/magnesium binding #status predicted 
F;530-538/Region: calcium/magnesium binding #status predicted 
F;530-501/Region: calcium/magnesium binding #status predicted 
F;1109-1134/Domain: transmembrane #status predicted <TMM>
F;1109-1134/Domain: intracellular #status predicted <TMM>
F;1135-153/Domain: intracellular #status predicted <TMM>
F;1135-153/Domain: transmembrane #status predicted <TMM>
F;1135
                                        RESULT 2
RWHULC
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A;Note: the last three bases of intron 13, CAG, are included in some but not all matur A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
R;Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mo1: conservation across A;Reference number: A90664; MUID:87076671; PMID:3539202
A;Accession: A26091
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A;Residues: 17-31 <PIE>
A;Experimental source: granulocytes
R;Pahl, H.L.; Rosmarin, A.G.; Tenen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:12059:
A; Map position: 16p11.2-16p11
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A;Molecule type: DNA
A;Residues: 1-9 <RES>
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A;Title: Characterization of the myeloid-specific CD11b promoter.
A;Reference number: I52567; MUID:92144986; PMID:1346576
A;Accession: I52567
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A;Residues: 1-499,501-1153 <FLE>
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         surface
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glycoprotein
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                                                                                                                                                                                                                                                                                                         VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 223
                                                                                                                                                                                                                                                                                                                                                                                                    DGEKFGDPLGYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT
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                                                                                                                                                                                                                             VNN-FEALKTIQNQLREK---
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         CD11c
    precursor
                                                                                                                                                                                                                        - IFAIEGTQTGSSSSFEHEMSQEGFSAA
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    C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
                                                                                                                                                                                                                        A40020
                                                                                                                                  N; Alternate names: fibrochimerin
                                                                                                                                                                           collagen alpha 1(XII) chain precursor -
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A;Map position: 16p11.2-16p11.2

C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol C;Superfamily: cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F;20-1107/Domain: extracellular #status predicted <EXT>
F;149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F;1108-1133/Domain: transmembrane #status predicted <TMM>
F;1134-1163/Domain: intracellular #status predicted <INT>
F;1134-1163/Domain: intracellular #status predicted <INT>
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A;Residues: 1-1163 <COR>
A;CORS-references: UNIPROT:P20702
A;CORS-references: UNIPROT:P20702
A;Note: this revision to the sequence from reference A35543 includes the R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit, the leukocyte p1
A;Reference number: A35543; MUID:90153906; PMID:2303426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830 A;Note: part of this sequence was confirmed by protein sequencing C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
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A;Cross-references: GDB:119758; OMIM:151510
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A; Residues: 1-755, 'L', 757-1163 <CO3>
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A; Residues: 1-834 < CO2>
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                                                                                                              SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND-----IASKPSQEHIFKVED-
                                                                                                                                                                                                                            NPLSLLASVHQLQ--
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                                                  FOALOGIIHSILKKSCIEILAAEPSTICAGESFOVVVRGNGF
                                                                                                                                                                       LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG
                                                                                                                                                                                                                                                                                  ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
FDALKDIQNQLKEK----IFAIEGTETTSSSSFELEMAQEGF
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my€

chicken

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A;Molecule type: mRNA
A;Residues: 2960-2976; F',2978-3074,'AG' <GOR3>
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A;Note: this sequence has been revised in reference A34485
R;Koch, M.; Bernasconi, C.; Chiquet, M.
Bur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified A;Reference number: $23814; MUID:92362621; PMID:1323460
A;Accession: $23814
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A,Title: The two splice variants of collagen XII share a
A,Reference number: S28811; MUID:93042014; PMID:1420368
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A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
R;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsish;Reference number: $22254; MUID:88087065; PMID:3121603
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A;Residues: 2772-2792;2846-2873 <GOR2>
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix (A;Reference number: A28037; MUID:87317590; PMID:3476925
A;Accession: A28037.
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A;Residues: 1-3124 <YAM>
A;Residues: 1-3124 <YAM>
A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:G222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:G222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P13944; GB:D00824; NID:g2222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:BAA00701.1; PIDN:BAA007
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A; Residues: 1-24, 1189-1257, 'S', 1259-1263, 'E', 1265-1280 <TRU>
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A;Title: The complete primary structure of type XII collagen shows a chimeric molecular region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp A;Reference number: A40020; MUID:92011862; PMID:1918137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S28811
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A;Title: Type XII collagen. A large multidomain molecule with partial homology to
A;Reference number: A34485; MUID:90062079; PMID:2584192
A;Accession: A34485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                    Aintrons: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1

Keywords: alternative splicing; cell binding; coiled coil; connective tissue;

71-23/Domain: signal sequence #status predicted <SIG-

724-3124/Product: collagen alpha I(XII) chain #status predicted <MAT-

724-114/Domain: IIIA #status predicted <IIIA-

724-114/Domain: IIIA #status predicted <IIIA-

724-114/Domain: tibronectin type III repeat homology <FN3A-

7332-301/Domain: Fibronectin type III repeat homology <VWA1-

7332-414/Domain: IIIB #status predicted <IIIB-

7332-414/Domain: fibronectin type III repeat homology <FN3B-

7332-141/Domain: Fibronectin type III repeat homology <FN3B-

7332-141/Domain: von Willebrand factor type A repeat homology <VWA2-

7437-601/Domain: Von Willebrand factor type A repeat homology <VWA2-

7437-1178/Domain: IIIC #status predicted <IIIC-
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,995-1076/Domain: fibronectin type III repeat homology <FN3G>,1086-1169/Domain: fibronectin type III repeat homology <FN3H>,1197-1361/Domain: von Willebrand factor type A repeat homology
                                                                                                                                                                  1630-711/Domain: fibronectin type III repeat homology <FN3C>
1721-802/Domain: fibronectin type III repeat homology <FN3D>
1812-895/Domain: fibronectin type III repeat homology <FN3E>
1905-986/Domain: fibronectin type III repeat homology <FN3F>
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,Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB;
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Fila84-1465/Domain: fibronectin type III repeat homology <FN3I>
Fil474-1557/Domain: fibronectin type III repeat homology <FN3I>
Fil665-1647/Domain: fibronectin type III repeat homology <FN3I>
Fil665-1738/Domain: fibronectin type III repeat homology <FN3I>
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Fil7937-2101/Domain: fibronectin type III repeat homology <FN3IP>
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Fil793-2490/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted <COL2>
Fil793-2902/Domain: cell adhesion #status predicted <COL2>
Fil793-2902/Domain: collagenous COL2 #status predicted <COL1>
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Fil7946-3048/Domain: collagenous NC2 #status predicted <COL1>
Fil7946-3048/Domain: collagenous NC2 #status predicted <CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukocyte surface glycoprotein Mac-1 alpha chain precursor N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_ch C;Accession: S00551; I59078
                                                                                                                                                                                        A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983 A;Note: the authors translated the codon CAC for residue 569 as Gln R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.B.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986 A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A;Reference number: 159078; MUID:86287312; PMID:2942940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 7, 1371-1378, 1988
A;Title: Amino acid sequence of the murine Mac-1 alpha chain A;Reference number: 800551; MUID:88312584; PMID:3044779
A;Accession: S00551
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                                         A; Molecule type: DNA
A; Residues: 11-44 < RES>
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        A;Cross-references:
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GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
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RESULT 5
A48569
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A;Title: Sequence of a major Eimeria maxima antigen homologous A;Reference number: A48569; MUID:93149203; PMID:8426611
A;Accession: A48569
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                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891
A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F;238-296/Domain: thrombospondin type I repeat homology <THR1>
F;309-371/Domain: thrombospondin type I repeat homology <THR2>
F;372-432/Domain: thrombospondin type I repeat homology <THR3>
F;474-456/Domain: thrombospondin type I repeat homology <THR5>
F;494-556/Domain: thrombospondin type I repeat homology <THR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Eimeria maxima
C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
C:Accession: A48569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom C;Keywords: cell adhesion; glycoprotein; transmembrane protein F;1-16/Domain: signal sequence #status predicted <SIG>
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Best Local (
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                                                                                      SDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDG
                                                                                                                                                                                                                       CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKL
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                                          ELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 234
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                                                                                                                                   TEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDG 125
                                                                                                                                                                               CTRLLDVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSFDDVRVGLVTFGTSAVTRWDL 101
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  SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPR
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26.6%;
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                                                                                                                                                                                                                                                                                        Score 139; DB 2
Pred. No. 0.003;
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A; Noticelle type: protein
A; Residues: 1551-1570;1593;1599;1639-1667 < GGR2>
A; Residues: 1551-1570;1593-1599;1639-1667 < GGR2>
C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycop
E; 40-204/Domain: von Willebrand factor type A repeat homology < VWA1>
F; 236-317/Domain: fibronectin type III repeat homology < FN3B>
F; 236-409/Domain: fibronectin type III repeat homology < FN3C>
F; 418-498/Domain: fibronectin type III repeat homology < FN3D>
F; 507-591/Domain: fibronectin type III repeat homology < FN3F>
F; 716-798/Domain: fibronectin type III repeat homology < FN3F>
F; 716-798/Domain: fibronectin type III repeat homology < FN3F>
F; 924-1089/Domain: von Willebrand factor type A repeat homology < FN3G>
F; 924-1089/Domain: non-collagenous NC4 #status predicted <NC4>
F; 1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F; 1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA, A;A36-1119,'KL',1122-1402,1409-1439 <TRU> A;Residues: 286-494,'Q', 496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU> R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: sequence extracted from NCBI R;Apte, S.S.
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A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide translation
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C;Date: 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, J. Biol. Chem. 268, 12177-12184, 1993
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A; Residues: 1472-1659 <GOR1>
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A; Residues: 1472-1660 < APT>
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A; Residues: 1-1747 <GER>
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                                                            926 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 985
                                                                                                                                                                                       63 ;
                                                                                                                                                                                                                   Similarity
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DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE
                                                                                                                        DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                             Score 137; DB 2
Pred. No. 0.014;
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                                                                                                                                                                                                                                             DB 2; Length 1747;
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RESULT 8
C2MS
Classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C2 (
N,Alternate names: C3 convertase; C5 convertase; complement C2
(,Species: Mus musculus (house mouse)
C,Bpecies: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change
C,Accession: A38876; B36593; T54429
R,Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R.
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A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
F;48-218/Domain: von Willebrand factor type A repeat homology <VWA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J. Mol. Blochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064; PMID:1775171
A;Accession: A45638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodominant microneme protein Etp100 - Eimeria tenella
C/Species: Eimeria tenella
C/Datci 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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                             A;Reference number: A38875
A;Accession: A38876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;238-296/Domain: thrombospondin type 1 repeat homology <THR1>;309-371/Domain: thrombospondin type 1 repeat homology <THR2>;309-371/Domain: thrombospondin type 1 repeat homology <THR3>;372-432/Domain: thrombospondin type 1 repeat homology <THR3>;433-491/Domain: thrombospondin type 1 repeat homology <THR4>;436-656/Domain: thrombospondin type 1 repeat homology <THR5>;560-610/Domain: thrombospondin type 1 repeat homology <THR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-712 <TOM>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                           153 VPKLVLVMTDGA--SNLPSQTRSSAAALRDAGAIVVVLGVGSGVNSSECRSIAGCSTSNC
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                                                                                                                                                                                                                                                                                                                                                                        P-----VNDGFQALQGIIHSILKKSCIEILAAEPSTI--CAGE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTSLLDVMLVVDESGSIGTSNFRKVRQFIEDFVNSMPISPEDVRVGLITFAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKL
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                                                                                                                                                                                                                                                                                                                               PRYLOSNWSNVTOOVNGIIKAACKDLAKDAVCSEWSEYGPCVGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEDREQIRQGLEELQKVLPG-----
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Pred. No. 0.00
40; Mismatches
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                                                                                                                                                                                                             component precursor
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                                              RESULT
S31212
collagen alpha 1(XIV) chain precursor,
C;Species: Gallus gallus (chicken)
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A; Introns: 16/1
C; Complex: The J
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: cleaves complement C3 and complement C5 alpha chains
A;Description: cleaves complement C3 and complement C5 alpha chains
A;Pathway: complement B/C2; complement factor H repeat homology; trypsin homology; vc
C;Keywords: alternative splicing; complement classical pathway; duplication; glycoproteir
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-2-89/Domain: complement C2b fragment #status predicted <C2B>
F;2-2-89/Domain: complement factor H repeat homology <FH2>
F;94-149/Domain: complement factor H repeat homology <FH2>
F;551-760/Product: complement factor H repeat homology <FH2>
F;251-760/Product: complement C2a fragment long form #status predicted <C2A>
F;251-60/Product: complement C2a fragment bhort form #status predicted <C2S>
F;251-449/Domain: von Willebrand factor type A repeat homology <VFA>
F;251-40/Domain: von Willebrand factor type A repeat homology <VFA>
F;478-747/Domain: trypsin homology #status atypical <TRY>
F;478-749/Domain: trypsin homology #status atypical <TRY>
F;279-136,123-136,122-139,156-197,182-210,470-590,499-515,593-609,647-674,685-715/Dist
F;27,117,297,340,474,478,663/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;514,570,689/Active site: His, Asp, Ser #status predicted
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J. Biol. Chem. 265, 19940-19046, 1990
A;Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different me A;Reference number: A36593; MUID:91035430; PMID:2229060
A;Accession: B36593
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A;Title: DNA polymorphism of MHC III genes in inbred and wild mouse strains.
A;Reference number: I54429; MUID:87192938; PMID:2883115
A;Accession: I54429
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A;Cross-references: UNII
R;Ishikawa, N.; Nonaka,
J. Biol. Chem. 265, 190
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A;Cross_references: GB:M16271; NID:g199289; PIDN:AAA39562.1; PID:g199290
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A; Residues: 660-677, 'R', 679, 681-723, 'G', 725
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Best Local
                                                             273
                                                                                                                       473
                                                                                                                                                                                 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
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                                                                                                                                                                                                                                                                                                                                                                       KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERSQ-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-----NRQGYRTAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILS
VGDPTSQHGKEFLVEDVII
                                                          MND----GLSFISSSVII
                                                                                                                                                                                 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 272
                                                                                                                                                                                                                                               LNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVSKL
                                                                                                                                                                                                                                                                                                         FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----
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                                                                                                                    GNMSANASDQERTPWQVTFKPKSKETCQGS--LISDQWVLTAAHCFHDIQMEDHHLWRVN
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                                                             286
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   549
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R; Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV. A;Reference number: S31211; MUID:93185668; PMID:8444186
                                                                                                                                                                                                                                                                                                                                                           RESULT 10
$78476
$78476
$collagen alpha 1(XIV) chain precursor, long form -
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence revision 17-Apr-1998
C;Accession: $78476; $31211
C;Accession: $78476; $31211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;352-433/Domain: fibronectin type III repeat homology <RN3B-
F;442-55/Domain: fibronectin type III repeat homology <RN3C-
F;534-614/Domain: fibronectin type III repeat homology <RN3C-
F;623-707/Domain: fibronectin type III repeat homology <RN3E-
F;741-823/Domain: fibronectin type III repeat homology <RN3F-
F;832-914/Domain: fibronectin type III repeat homology <RN3G-
F;932-1009/Domain: fibronectin type III repeat homology <RN3H-
                          A;Reference number: S31211;
A;Accession: S31211
A;Status: preliminary
                                                                      Eur. J. Blochem. 414, 455-450, 200
A;Title: Complete primary structure of chicken collagen XIV
A:Reference number: 831211; MUID:93185668; PMID:8444186
                                                                                                                                   A;Residues: 1-1888 <TRUNA;Cross-references: UNIFOCT:P32018; EMBL:X70793; NID:9288872; PIDN:CAA50064.1; R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Eur, J. Biochem. 212, 483-490, 1993
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F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted
F;29-110/Domain: fibronectin type III repeat homology <FW3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
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A; Residues: 1-1857 < WAE>
A; Cross-references: EMBL:X70792; NID:g288874;
A; Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: S31211; MUID:93185668; A;Accession: S31212
A; Molecule
                                                                                                                                                                                                                                                                                  A;Reference number: S78476
A;Accession: S78476
                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Gene: Col14A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;1040-1205/Domain: von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Keywords: alternative splicing; coiled coil;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 1101
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25.0%; Pred. No. 0.055;
tive 44; Mismatches 116; Indels 2
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                                                                                                                                                                                                                                                                                                                                         January 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extracellular matrix; glycoprotein;
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                                                                                                                                                                                                PID:g2888
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F;1-28/Domain: signal sequence #status predicted <SIGS
F;29-1988/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWAl>
F;352-433/Domain: fibronectin type III repeat homology <FN3S>
F;442-525/Domain: fibronectin type III repeat homology <FN3S>
F;442-525/Domain: fibronectin type III repeat homology <FN3S>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;741-823/Domain: fibronectin type III repeat homology <FN3G>
F;731-93/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3H>
F;812-1009/Domain: fibronectin type III repeat homology <FN3H>
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S42373
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A;Cross-references:
C;Genetics:
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C;Keywords: alt
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A; Residues: 1-3051 < SMI >
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                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 96/1; 166/3; 201/2; 355/1; 404/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T20G5.3 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Caenorhabditis elegans;Date: 07-Oct-1994 #sequence_revision
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                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
ELFEIGRSKTRVGLIQYSDQIRHEFDLDQYGDRDSLLKGISETQ-YLTGLTRTGAAIQHM
                                             HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                     CYGGFVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVFKNEVLRFVREFV 542
                                                                                                                                                        CYGGF---
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25.0%; Pred. No. 0.05
tive 44; Mismatches
                                                                                                                                                                                                  8.3%; Score 128; DB 2; Length 3051; 27.1%; Pred. No. 0.16; tive 31; Mismatches 75; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March
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0.057;
                                                                                                                                                        -DLYFILDKSGSVLHH--WNEIYYFVEQLA 44
                                                                                                                                                                                                                                                                                                                                                                                        427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GFKMMEMFGLVEKEFSAIDGVSMEPGTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Cartilage matrix protein precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004 C;Date: 12-Jul-1999; B37979 C;Accession: A37979; B37979 S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh J. Biol. Chem. 265, 19624-19631, 1990 J. Biol. Chem. 265, 19624-19631, 1990 A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix A;Reference number: A37979; MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
A37979
A;Molecule type: mRNA
A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1;
                                                                                                                 A;Residues: 1-496 <JEN>
A;Cross-references: UNIPROT:P21941;
                                                                                                                                                                                                 A; Reference number: A37979;
A; Accession: A37979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-8ep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                        A; Accession: B37979
                                                                                                                                                                     A, Molecule type: DNA
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F/155-236/Domain: fibronectin type III repeat homology <3FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-929 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. 168,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y.; Yang, b...
168, 503-513,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 DIVLLVDGSWSIGRPNFKIVRNFISRVVEVFDIGSDRVQIAVSQYSGDPRTEWQLNTHKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVAPSKRYA----DEGIELYAVGIKNADENELKEIASDPDELYMYNVADFSLLTNIVNDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---QEVYVRGTQTTTVLVGLKPETEYYVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSVEDTYLLCPAPILKEVGMKAALQVSMN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E.V.; Klatt, K.P.; Tassava, R.A.
503-513, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 118; DB 2; Length 929; 21.2%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
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                                                                                                                 GB:J05667
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A;Molecule type: mRNA
A;Residues: 467-546;550-595;752-764 <WOO>
A;Cross-references: GB:J00185; GB:J00186
A;Note: the authors translated the codon TAC at 519 as Thr; tl
A;Nole; J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
Clem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human a;Reference number: A20751; MUID:84161997; PMID:6546754
A;Accession: A00934
R;Christie, D.L.; Gagnon, J.
Biochem. J. 209, 61-70, 1983
A;Title: Amino acid sequence
                                                                                                                                                                         A; Molecule type: protein; mRNA
A; Residues: 26-764 < MOL>
A; Cross-references: GB: K01566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN:CAA51389.1; R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R. Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein factor B, a A;Reference number: A44622; MUID:83039428; PMID:6957884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 09-Ju
C;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971;
R;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
submitted to the EMBL Data Library, March 1993
A;Reference number: S34075
A;Accession: S34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement factor B precursor [validated] - human
N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-]
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
                                                                                                                  A;Note: nucleic acid translation differs A;Note: 736-Ser was also found
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                                                                                   A; Note: glycosylation sites were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A44622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-764 < MEJ>
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F;39-206/Domain: von Willebrand factor type A repeat homology <VWA1>
F;227-262/Domain: EGF homology <EGF>
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C; Superfamily: cartil
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A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: cartilage matrix protein; EGF homology; von
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS--KDHVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEFPLGRFHTKKDİKAAVRNM-----SYMEKĞTMTGAALKYLIDNSFTVSSGARPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYGG-----FDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMSFIV---FSTR
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26.0%; Pred. No. 0.2;
tive 35; Mismatches
                                                                                         determined
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A;Molecule type: mRNA
A;Residues: 339-509 <CAl>
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
R;Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
Cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human complement protein factor B gene: evidend A;Reference number: A25971; MUID:87102880; PMID:3643061
A;Accession: B25971
                                                                                                              A;Map position: 6p21.3-6p21.3
A;Map position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3;
A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein A;Residues: 270-329 <NIE> A;Residues: 270-329 <NIE> A;Residues: 270-329 <NIE> A;Residues: 270-329 <NIE> A;Rote: binding site for carbohydrate to lysine under artificial conditions A;Morley, B.J.; Campbell, R.D. EMBO J. 3, 153-157, 1984 EMBO J. 3, 153-157, 1984 A;Reference number: A44628; MUID:84158524; PMID:6323161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Campbell, R.D.; Porter, R.R. Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983 Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983 A;Title: Molecular cloning and characterization of the gene coding for human complement A;Reference number: A19947; MUID:83273641; PMID:6308626 A;Accession: A19947
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-31,'Q',33-764 <RE2>
A;Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1;
C;Comment: 292-Cys has a free sulfhydryl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 16-225,'F',227-259 <MOR>R;Schwaeble, W.; Luttig, B.; Sokolowi
Immunobiology 188, 221-232, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Niemann, M.A.; Bhown, A.S.; Miller, E.J.
Blochem. J. 274, 473-480, 1991
A;Title: The principal site of glycation of human complement A;Reference number: S14339; MUID:91174758; PMID:2006911
A;Accession: S14339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Human complement factor B: cDNA cloning, nucleotide A;Reference number: I57824; MUID:94067177; PMID:8247029 A;Accession: I57824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Human complement factor B: functional properties of a recombinant zymogen A;Reference number: I54409; MUID:94041399; PMID:8225386 A;Accession: I54409
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A;Residues: 1-99 <WUL>
A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
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A;Contents: the final paper in a series documenting the sequence, glycosylation site,
                                                                     A;Description: Bb is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-764 < RES>
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                   ;Gene: GDB:BF
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ol. Immunol. 30, 1587-1592, 1993
                                                                                                                                                                                                                                                                                                                             Cross-references: GDB:119726; OMIM:138470
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                                                                 serine proteinase;
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C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc(;Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrolafication; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; complement factor H repeat homology cFH1>
F;103-158/Domain; complement factor H repeat homology cFH2>
F;165-218/Domain; complement factor H repeat homology cFH3>
F;268-458/Domain; complement factor H repeat homology cFH3>
F;268-458/Domain; complement factor type A repeat homology cVFA>
F;482-752/Domain; trypsin homology #status atypical cTRY>
F;482-752/Domain; trypsin homology #status atypical cTRY>
F;482-752/Domain; trypsin homology #status atypical cTRY>
F;482-752/Bomain; trypsin homology #status atypical cTRY>
F;37-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Diff;259-260/Cleavage site; Arg-Lys (complement factor D) #status experimental
F;259-260/Cleavage site; Arg-Lys (complement factor D) #status experimental
F;526,576,699/Active site; His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-2944 <CHR>
A;Residues: 1-2944 <CHR>
A;Residues: 1-2945 <CHR>
A;Cross-references: UNIPROT;Q02388; GB:L02870; NID:g987124; PIDN:AAA;
R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem, Biophys. Res. Commun. 183, 958-963, 1992
A;Title: Molecular cloning and characterization of type VII collagen
A;Reference number: PH0844; MUID:92231902; PMID:1567409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text chang
C;Date: 04-Nov-1994 #sequence revision 04-Nov-1996; I84686
C;Accession: A54849; PHO844; S16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
Tibiol. Chem. 269, 20256-20262, 1994
A;Tibiol. Chem. 269, 20256-20262, 1994
A;Tibiol. Cloning of human type VII collagen. Complete primary
A;Reference number: A54849; MUID:94327588; PMID:8051117
A;Accession: A54849
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A54849
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Baue: Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
                                                                                                    A;Molecule type: mRNA
A;Rosidues: 'E75,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C',
A;CROSE-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699
A;Experimental source: keratinocyte
A;Experimental source: keratinocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 YGVKP--RYGLVTYATYPKIWVKVSEADSSNADWVTKQLNEINYEDHKLKSGTNT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 EGVDAEDGHGPGEQQKRKIVLDPSGSMNIYLVLDGSDSIGASNFTGAKKCLVNLIEKVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 KFISPOLRMSFIVFSTRGTTLMKLTE----DREQIRQGLEEL----QKVLPGGDTYMHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QGGRREDG-GPA------CYGGFDLYFILDKSGSV-----LHHWNEIYYFVEQLAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REANRSRDIGATVYCVG--VKDFNETQLARTADSKDHVFPVNDGFQALQGTIHSILKKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KKALQAVYSMMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QSLSLC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113.5;
Pred. No. 0.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GMVWEHRKGTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527
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                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: AAA75438.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YHKQPWQAKISV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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                                       K.C.; Bauer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                              E.A.;
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F,864-952/Domain: fibronectin type III repeat homology <FN9>
F,954-1045/Domain: fibronectin type III repeat homology <FN9>
F,954-1045/Domain: von Willebrand factor type A repeat homology <VWA2>
F,1052-1219/Domain: von Willebrand (R-G-D) motif
F,1189-1253/Region: cell attachment (R-G-D) motif
F,1254-2783/Region: cell attachment (R-G-D) motif
F,1254-2783/Region: cell attachment (R-G-D) motif
F,1234-1336/Region: cell attachment (R-G-D) motif
F,2500B-2010/Region: cell attachment (R-G-D) motif
F,2553-2555/Region: cell attachment (R-G-D) motif
F,25784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F,2784-2944/Domain: animal Kunitz-type proteinase inhibitor homology <BD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 2395-2871'.8',2873-2944 <REZ>
A;Residues: 2395-2871'.8',2873-2944 <REZ>
A;Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g388714
A;Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g388714
R;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a (A;Title: Dominant dystrophic epidermolysis bullosa: identification of a (A;Reference number: A55255; MUID:94224777; PMID:8170945
A;Contents: annotation
C;Comment: Prolines and lysines at the third position of the tripeptide of and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C/REYWORDS: CO11ed CO11; extracellular matrix; glycoprotein; hydroxyly F;17-16/Domain: signal sequence #status predicted <SIG> F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
A;Note: there are 118 introns
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A;Title: The carboxyl-terminal half of type VII collagen, A;Reference number: I48103; MUID:93271985; PMID:8499916
A;Rccession: I84686
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.
J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles
A;Reference number: 156328; MUID:93107742; PMID:1469284
A;Accession: 156328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NJOULISET, J.L.; Bisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.I. Biol. Chem. 264, 3822-3826, 1989
NJTitle: Cleavage of type VII collagen by interstitial collagenase and NReference number: A30296; MUID:89139437; PMID:2537292
NGlacvic ****
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,;Gene: GDB:COL7A1; EBR1; EBD1; EB
,;Gene: GDB:128750; OMIM:120120
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,Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E',2032,'C',2034-2041,
,Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description: structural component of extracellular polymer; Reywords: coiled coil; extracellular matrix; glycoprotein;
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Cross-references: GB.M65158; GB.S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1; PID:g262309 Glanville, R.W.; Burgeson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  including the non-collagenous
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                                                                                                                                                                                                                                                                                                                        Matches
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                                                                              154
210
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                                                                                                                    130 DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH 187
                                                                                                                                                                                                  70
                                                                                                                                                           98 GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                                                          38 DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL 97
                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                  TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE 129
                                                                                                                                                                                                                                                                               DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
LVSRRVCTTAGGVPVTRPPDDSTSAPRDLVLSEPSS
                                                                            DLV---DTAAQRLKGQGVKLFAVGIKNADPEBLKRVASQPTSDFFFFVND-FSILRTLLP 209
                                                                                                                                                                                                                                                                                                                      Conservative
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                                       -----BILAAEPST 204
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Search completed: June 13, time

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Result
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1 Human in f
8 Human TAN
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ALIGNMENTS

## Region Region Region Region Region Region 08-JAN-2003 ABP54903; WO200246228-A2 Domain Domain Anthrax; toxin; ABP54903 standard; protein; 368 Domain Protein Peptide Homo sapiens. Human anthrax toxin receptor (first entry) receptor; human; antibacterial. /note= /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 52, 54 and 118" 320. .343 /note= "PA-binding fragment, begins at any amino acid in the range 27-43 and ends at any amino acid in the range 221-321, region specifically described in Claim 3" /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 52, 54 and 150" motif with /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 54, 118 and 150" /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 52, 54, 118 and 150" 28. .320 /note= "extracellular domain" 28. .368 Location/Qualifiers /note= "forms metal ion-dependent adhesion notif with amino acid residues 50, 52, 118 note= "von Willebrand factor A domain" label= Mature\_protein label Signal peptide "cytoplasmic domain" "putative transmembrane domain" ₿ site (MIDAS) and 150"

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RESULT 2
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   Human;
                                 Human gene 4
                                                                 17-JUL-2001
                                                                                                 AAE01439;
                                                                                                                              AAE01439 standard; protein; 403 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 29-30; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polypeptide useful for identifying agent that prevents or reduces effect of anthrax toxin on host cell, for treating human or non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young
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DB; ABV73881.
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                              encoded secreted protein HWLFR02,
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                                                                (first entry)
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Pred. No. 1.5e-155;
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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted CC AAD05301-AAD05379 represent human secreted proteins they encode. CC AAB01514-AAB01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating cor ameliorating medical conditions, e.g., by protein or gene therapy. CC pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in CC the new genes. Specific uses are described for each of the 28 genes, the new genes. Specific uses are described for each of the 28 genes, cadeveloping products for the diagnosis or treatment of proliferative CC disorders, cancer, tumours, foetal and developmental abnormalities, can disorders, cancer, tumours, foetal and developmental abnormalities, communosis (e.g., rhemmatoid arthritis), inflammation, allergies, autoimmune constitute disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., pregnancy-related disorders, atherosoclerosis, cardiovascular disorders, gregnancy-related disorders, and combeton, and infections. The proteins can also be used to aid wound healing and epithelial cell correspondents, and infections. The proteins can also be used to aid wound healing and epithelial cell correspondents, and inchmotary tissues, to regenerate tissues, to identify their cognate ligands or binding correspondents, and in chemotaxis, and can be used as a food additive or prace properties and pribadies generific for a properties and inchmotaxis, and can be used as a food additive or prace properties.
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N-PSDB;
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                                                                               preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules encoding 28 human secreted proteins diagnosing, preventing, treating or ameliorating medical condit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999; 99US-0163581P.
30-JUN-2000; 2000US-0215133P.
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                                           radioimmunoassay
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                              a, and in diagnostic immunoassays e.g., immunosorbent assay (ELISA). The
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Sequence 403 \$

100.0%; Score 1526; 멂 4 Length 403;

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RESULT 3
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Matches
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25-APR-2000;
21-DEC-2000;
                     The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; cytostatic; anti-HIV; antidiabetic; haemostatic; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          albumin fusion protein; cytostatic; antianaemic; antiarthritic; antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory; antipsoriatic; antibacterial; osteopathic; dermatological; antisout; immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic; nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer; antidiabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer; reproductive system disorder; therapeutic protein.
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                                                                                                                                                                                                                                                                                                                                                 12-APR-2001;
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No. 1.8e-155;
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albumin fusion proteins,

useful for diagnosing,

treating,

preventing

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asthma,
                                                                  amellorating diseases or disorders e.g. cancer, anemia, arthritis, than, inflammatory bowel disease or Alzheimer's disease.
SEQ ID NO 621; 279pp; English.
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CC fragment or variant; a nucleic acid molecule comprising a polynucleotide comprising the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The CC albumin fusion protein and its compositions have the following cc activities: cytostatic, antianaemic, antiarthritic, antiarthratic, antiparting, antispendic, nephrotropic, uropathic, cc ardiant, nootropic, antilipaemic, nephrotropic, uropathic, anabolic, hypertensive, and vulnerary. The albumin fusion protein antiarthratic, anabolic, hypertensive, and vulnerary. The albumin fusion protein and colon, because of albumin fusion protein is cc useful for disgnosing, treating, preventing or ameliorating diseases or disorders comprising indication: Y. The diseases or disorders include: cc ancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), cc lamune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS, cc laydig tumours, musculoskeletal disease, psoriasis or Lyme CC laydig tumours, musculoskeletal disease, cy, giant cell tumours, actemic lunguar dystrophy stemic and disease, seventender and disease, acute and adenocarcinoma or Sertoli-Sachs disease), excretory diseases (e.g. urinary incontinence, urinary tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis, cerebellar ataxia, attention deficit disorder, autism or obsessive compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, sclaroderma, wound healing or epitermolysis bullosa). This sequence represents a therapeutic protein X relating to the albumin fusion protein of the invention. The sequence listing data for this specification was dowloaded from the USPTO website. Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy or cachexia), cardiovascular disease (e.g. rhabdomyomas, heart disease, arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome, Down's syndrome, Patau syndrome, Turner's syndrome, Apart syndrome or Tay Sachs disease), excretory diseases (e.g. urinary incontinuous) disorder in a patient comprising the step of administering the albumin fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of extending the shelf life of Therapeutic protein: X, or its; further relates to: a composition comprising the albumin fusion protein and a pharmaceutical carrier; a kit comprising the composition of the albumin fusion protein formula; a method of treating a disease or novel albumin fusion protein. invention

Sequence 403

Matches Query Match Best Local

293;

Conservative

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Similarity

100.0%;

Score 1526; DB 8; Pred. No. 1.8e-155; ; Mismatches 0;

Indels Length

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                                                                  The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and metho may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig mutated fusion protein of the invention.
                                              Sequence
                                                                                                                                                                 Claim 45;
                                                                                                                                                                                                  New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion; von Willebrand factor A-like domain; vWF; antibacterial; cutaneous; inhalation anthrax; human; TANGO 197 Ig fusion; mutan plasmid pO610; mutein.
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                                                                                                                                                                                                                                                                ameliorating domain (vWF) to the vWF.
                                                                                          The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising mouse TANGO197 and immunoglobulin (19) that can be used to treat exposure to or prevent a symptom of
                                                                                                                                                                                                                                                                         New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous
                                                            Sequence
                                                                                                                                                                                                                                        Claim 44; SEQ ID NO 18; 64pp; English
                                                                                                                                                                                                                                                                                                                                             WPI; 2003-829643/77.
                                                                                                                                                                                                                                                                                                                                                                      Rottman
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(HEAL/)
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Local 293;
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amino acid
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factor A-like domain amino acid sequence;
sequence; anthrax; Bacillus anthracis; cutaneous
hrax; mouse; TANGO197; immunoglobulin; Ig; fusion
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11-AUG-2000;
11-APR-2001;
The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90730, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cyrostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour growth, neoanglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psortiasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy: rhawman-
                                                                                                                                                                                                                                                                                                                                                                                      An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                          Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; nocangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial markers (NEM) (PEM) ABL91903-ABL91995
The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain tumour endothelial marker (TEM) protein selected from ABB90732, ABB9
                                                                         An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Tumour
                                                  Disclosure; Page 136-137; 331pp; English
                                                                                                                                                       St Croix B,
                                                                                                                                                                                                                      02-AUG-2000;
11-AUG-2000;
                                                                                                                                                                                                                                                           01-AUG-2001; 2001WO-US024031.
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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ilarity 100.0%;
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2000US-0224360P
2001US-0282850P
                                                                                                                                                        Kinzler
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                                                                                                                                                                                 JOHNS HOPKINS
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2.9e-155;
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                                  03-OCT-2001; 2001WO-US030941.
                                                                                                                                                                                     Domain
                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                      Anthrax; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human anthrax toxin receptor
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                                                                   13-JUN-2002
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                                                                                                                                                                                                                                    "extracellular domain"
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Pred. No. 2.9e-155;
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05-DEC-2000; 2000US-0251481P

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RESULT 10
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XX 12-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc anthrax toxin receptor (ATR), previously designated TEM8, and identified CC following a database screening using a newly isolated human surface-bound CC ATR (see ABP54903). The present sequence differs from the newly isolated CC human ATR only in the cytoplasmic domain (221 rather than 25 amino acids CC long), suggesting differential splicing of a primary mRNA transcript. CC Anthrax toxin protective antigen (PA) binds to these ATRs at a von CC willebrand factor A domain located in the extracellular domain of ATR. CC The invention provides ATR polypeptides and polynucleotides, vectors, CC host cells, and transgenic and knock-out animals. It also provides CC methods for identifying molecules that bind the ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a CC human or animal involves administering an agent that inhibits binding CC between PA and ATR at a level effective to reduce the severity of fragment of it, a PA-binding polypeptide at least 80% identical to these, a fusion protein, a monoclonal or polyclonal antibody, a polysaccharide, CC a lipid or a nucleic acid
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Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis;
                                                                        Human tumour endothelial marker TEM 19
                                                                                                             12-MAR-2003
                                                                                                                                                                                  ABU54457
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Pred. No. 2.9e-155;
Mismatches 0;
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N-PSDB;
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06-FEB-2002;
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Pred. No. 2.9e-155;
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06-FEB-2002; 2002US-0354262P.
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Huntington's disease; osteoarthritis;
Leber's hereditary ontic
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17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
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CC This invention relates to novel mitochondrial targets that can be used CC for therapeutic intervention in treating a disease associated with CC altered mitochondrial function. Specifically, it refers to a method for CC identifying proteins of the human heart mitochondrial proteome that are CC useful for drug screening assays, as well as therapeutic targets. The CC gresent invention describes a method for identifying such proteins that CC can be used in the treatment of various diseases associated with altered CC mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (IHON), mitochondrial CC encephalopathy lactic acidosis and stroke (MERAS), myoclonic epilepsy capged red fibre syndrome (MERRF) or cancer. Accordingly, these CC compositions have neuroprotective, nootropic, antidiabetic, captositatic acidosit should be controled to anticoroulsant, antiatrhritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart CC mitochondrial protein of the invention.

Sequence 564 A

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The present invention describes a method for detecting a pancreatic concer-associated transcript in a biological sample. The method comprises contacting the biological sample with a polynucleotide that selectively hybridies to a sequence at least 80% identical to a sequence as shown in any one of Tables 3 to 25 in the specification or having the GenBank CA Accession Number AP279145. Also described: (1) diagnosing pancreatic cancer in a human or animal subject being tested, determining the CC determining the subject having a pancreatic cancer will survive, or CC determining the subject having a subject having a pancreatic cancer for csurgical resection therapy; (2) detecting a pancreatic cancer-associated concer-associated transcript has cytostatic cancer. A pancreatic cancer—associated transcript has cytostatic cancer. A pancreatic cancer—associated transcript has cytostatic cancer associated transcript has cytostatic cancer—associated transcript concer-associated, a vector comprising the polynucleotide, an isolated concerning the polynucleotide, a vector comprising the polynucleotide, an isolated concerning the polynucleotide, an isolated concerning the polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting pancreatic cancer-associated transcript in a biological sample, useful for diagnosing or treating the disease, comprises contacting the sample with a polynucleotide that selectively hybridizes to a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;
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                                Misc-difference
                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene 4 encoded secreted protein HWLFR02,
                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted protein; proliferative disorder; cancer; tumour; abnormality; developmental abnormality; haematopoietic di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           μ
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                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
  /label=
                                                       note= "Encoded"
                                                                                                                                                                       label= Unknown
                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                        'label= Signal_peptide
                                                                                     label=
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                                                                                                                                         "Encoded
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                                                                                  Unknown
  Unknown
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Pred. No. 2.9e-155;
; Mismatches 0;
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/note=

"Encoded by

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CC AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted CC protein genes, and AAE01436-AAE01513 represent the proteins they encode. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating CC or ameliorating medical conditions, e.g., by protein or gene therapy. CC protein in a sample or by determining the amount of the comparison of the tissues in which they are most highly expressed, and include the new genes. Specific uses are described for each of the 28 genes, assed on the tissues in which they are most highly expressed, and include CC developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, cCC orginitive disorders, kidney disorders, gastrointestinal disorders, candiovascular disorders, cognitive disorders, kidney disorders, gastrointestinal disorders, ccc angiogenic disorders, kidney disorders, gastrointestinal disorders, ccc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to aid wound healing and epithelial cell cc protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., cradioimmunoassays or enzyme linked immunosorbent assay (EIJSA). The invention can a house a forested invention of the invention of a human socrated protein of the invention.
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 505-506; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1999; 99US-0163581P.
30-JUN-2000; 2000US-0215133P.
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LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA 180
                                                                                                                                     RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120
                                                                                                                                                                                                                                                                   QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403
                                                                                                  RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA
                                                                                                                                                                                                                                 QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                            Score 1515; DB 4;
Pred. No. 2.7e-154;
0; Mismatches 1;
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Matches 291; Query Match

Local

Similarity

99.3%; 99.7%;

Score 1515; DB 5; Pred. No. 2.7e-154;

Length 403;

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Gaps

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Conservative

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Mismatches

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AB663873
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PT AB613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albumin fusion protein; therapeutic protein X; human albumin; HA human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                           The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and disgnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, reproductive disorders (e.g. Alzheimer's, entingitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lon protein for treating disease e.g.
fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
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Result
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Perfect score:
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Maximum Match 100%
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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US-08-362-652-46
US-08-485-672-46
US-08-605-672-46
US-08-943-363-46
US-09-193-043-46
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US-09-350-259-46
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US-09-368-307A-53
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US-08-945-618-37
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US-08-945-618-37
US-08-945-632-37
US-08-945-333-37
US-08-945-333-37
US-08-945-333-37
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ALIGNMENTS

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GENERAL INFORMATION:
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                       Matches
                                     Query Match 10.9%;
Best Local Similarity 28.2%;
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,889

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

ATTORNEY/ACENT INFORMATION:

NAME: Williams Jr., JOSEPh A.

REGISTRATION NUMBER: P38,659

REFERENCE/DOCKET NUMBER: 27866/32168
                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
AADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5470953el Human
NUMBER OF SEQUENCES: 51
                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                               TELEPAX: 31.
TELEPAX: 25-3856
                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
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CITY: Chicago
                                                                                                                                                                       ENGTH:
                       66;
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                       Conservative
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                     42; Mismatches
Score 166; DB 1; Leng....
Pred. No. 6e-09;
Indels 30;
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acid
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                                                                                  Matches
                                                                                                   Query Match
Best Local :
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
FROME OF REQUENCES: 103
                                                                                                                                                                                                                                                                                                                                             NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REGISTRACE/DOCKET NUMBER: 2786: TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 5-AUG-1994
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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CURRENT APPLICATION DATA:
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CTTY: Chicago
TTY: Tlinof
                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312-474-63
TELEFAX: 312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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No. 5728533
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                                                                                                     Similarity
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                                      PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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  PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                                                                  Conservative
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                                                                                                                                                                                 protein
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                                                                              10.9%; Score 166; DB 1; Length 1155; 28.2%; Pred. No. 6e-09; tive 42; Mismatches 96; Indels 3
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Patent No. 5766850
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE Management
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0: FILING DATE: 23-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0: FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
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STREET: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                              144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                                                                                                                                                                                                                                                                                                 amino acid
                                                                       LTEDR----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
                                                                                                                                               PACYG-GFDLYFILDKSGSV-LHHWNEIYYFYEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                      FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                   312-474-6300
                                                                                                                                                                                     10.9%; Score 166; DB 1
28.2%; Pred. No. 6e-09;
ative 42; Mismatches
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cker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                          DB 1; Length 1155;
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US-08-605-672-46
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US-08-605-672-46
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Matches
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Best Local Similarity
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FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/:
APPLICATION NUMBER: US 08/:
APPLICATION NUMBER: US 08/:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING LALLON DATA:
PRIOR APPLICATION UMBER: US 08/286,889
APPLICATION NUMBER: US 08/286,889
PILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,67
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APPLICANT: Van der Vieren, Monica
TITLE OP INVENTION: NO. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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5817515
                                                                         TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                                LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIJAL 121
                                                                                                                                                                                                                                                                                                                 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.9%; Score 166; DB 2; Length 1155;
28.2%; Pred. No. 6e-09;
tive 42; Mismatches 96; Indels 3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/ACENT INFORMATION:
ANALYSIS AND AUGUST AUGUS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 23-DEC-PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/173,497
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 5831029el Human
NUMBER OF SEQUENCES: 103
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TELEFAX: 312-474-0448
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                             68 LTBDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
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PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                     TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                                                                                      TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                                                                                                                                                  PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                                                                                                                    PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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3 South Wacker Drive, 6300 Sear Tower
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Pred. No. 6e-09;
2; Mismatches
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US-08-943-363-46
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                                                                                                                                                                                                                                                                                          Matches
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-4'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                         122 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                             204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
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TYPE: Floppy disk
 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
                                                                       TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                                                                                                                                                                   PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                     PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive, 6300 Sear Tower

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Pred. No. 6e-09;
42; Mismatches
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 364
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; TYPE: PRT
; ORGANISM: Mus
US-09-193-043-46
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EARLIER FILING DATE: 1993-12-33
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6432404 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Best Local Similarity
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                                                                                                                                                                                                               APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
                                                                                                                             PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
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APPLICATION
FILING DATE:
                                                                                  APPLICATION NUMBER: 08/286,889 FILING DATE: 1994-08-05
                                         FILING DATE:
                                                               APPLICATION NUMBER: 08/362,652
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5. 6251395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
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; ORGANISM: Mus musculus
US-09-350-259-46
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US-09-350-259-46
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46
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CURRENT APPLICATION NUMBER: US/09/350,259

CURRENT FILING DATE: 1999-07-08

EARLIER APPLICATION NUMBER: 09/193,043

EARLIER FILING DATE: 1998-11-16

EARLIER APPLICATION NUMBER: 08/173,497

EARLIER FILING DATE: 1993-12-33

EARLIER FILING DATE: 1993-12-39

EARLIER FILING DATE: 1994-08-05

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Application US/09350259 Patent No. 6620915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915el Human 2
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                       Local
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                                                                                   204 FTBFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                        144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                                                                                                                                                                                                                                                                                                                                                                                                      1155
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                                                                                                                                                                                                                                                                                       Similarity
                                       TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
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                                                                                                                            LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIJAL 121
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TDGOKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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Pred, No. 6e-09;
"'' Thatches 96; Indels
                                                                                                                                                                                                                                                           Score 166; DB 4; L
Pred. No. 6e-09;
42; Mismatches 96;
                                                                                                                                                                                                                                                                                                       DB 4; Length 1155;
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                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
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                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Williams Jr., JOSEPh A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKST NUMBER: 2786
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
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TITLE OF INVENTION: No. 5728533el Human
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                    FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                              TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                                      PACYG-GFDLYFILDKSGSV-LHHWNBIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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                                       TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive, 6300 Sear Tower

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21-DEC-1994
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28.2%;
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                                                                                                                                                                                                                                                                             Score 166; DB 1;
Pred. No. 6e-09;
2; Mismatches 96
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316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD

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RESULT 12
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER READAB!
MEDIUM TYPE:
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
TITLE OF CENTENCES: 93
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CTTY: Chicago
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REFERENCE/DOCKET NUMBER: 2786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 60606-6402
MPUTER READABLE FORM:
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Local Similarity 28.2%;
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                                                                                                173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
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                                                                                                                                                                              122 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                        204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSÄKKILIVI 258
                                                                                                                                                                                                                                                           68 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIJAL 121
                                                                                                                                                                                                                                                                                                                                           10 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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5766850
                                                          KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
                                                                                                                                          TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                                                                                                                                                                                                                                                   PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive, 6300 Sear Tower

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                                                                                                                                                                                                                                                                                                                                                                                   42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Score 166; DB 1; Length 1161;
Pred. No. 6e-09;
42; Mismatches 96; Indels 3
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US-08-482-293A-53
; Sequence 53, Application US/08482293A
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                                          RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
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CITY: Chicago
Illinois
"""" "mited
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                   316
                                                                                                                                      173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                                                                                                                                                                                                     204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                             144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                        68 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
66; Conserv
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                                                                                                                                                                                                                TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                                                                                                                                                              PACYG-GFDLYFILDKSGSV-LHHWNBIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK
                                                                                                 KVGN-FVALRSIOROIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                             TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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28.2%; Pred. No. 6e-09;
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RESULT 14
US-08-943-363-53
J Sequence 53, Application US/08943363
J Patent No. 5837478
J Patent No. 58374770N;
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Best Local Similarity
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GENERAL IN
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: 4111457 7- TORONA
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SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
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REFERENCE/DOCKET NUMBER: 2786
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 60606-6402
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STATE: Illinois
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233 South Wacker Drive, 6300 Sear Tower
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Pred. No. 6e-09;
12; Mismatches 96; Indels 3
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RESULT 15 US-09-193-043-53

GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica Sequence 53, Application US/09193043 Patent No. 6251395 S

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US-08-943-363-53
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
US 08/173,497
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION: No. 5837478el Human
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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STATE: Illino
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                                                                                                                       122
                                     173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                                                                                                               204
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                                                                                                                                                                                                   68 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
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KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                   TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF
                                                                                                                                                             FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
                                                                                                                                                                                                                                             PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
                                                                                                                                                                                                                                                                                   PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK
                                                                             TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                                                                            10.9%; Score 166; DB 2 28.2%; Pred. No. 6e-09;
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FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIAN NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIAN NUMBER: 08/943,363
LENGTH: 1161
TYPE: PAT
CORGANISM: Mus musculus
US-09-193-043-53
Search completed: June 13, 2005, 20:05:08 Job time: 29.4879 secs
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                                                                                                                                              173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                                                                                                                                                                                        122 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                                                                                                                                                                                            316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                    259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                                                                                                                                                                                                                                                  204 FTÉFKSSLSPQSLVDAIVQÍQ-----GLTÝTASGIQKVVKELFHSKNGARKSÁKKILÍVI 258
                                                                                                                                                                                                                                                                                                                            68 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
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No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                                                                                              Score
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                                                                                                                          1526
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1526
1526
                                                                                                                                                                                                                                                                                                                                             derived by analysis of the total score distribution.
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                                                                1000.
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Gapop 10.0 , Gapext 0.5
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1526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO0E_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO0E_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO0E_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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5644
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10
14
16
                                                            US-09-833-245-621

US-10-038-307-18

US-10-201-292-18

US-09-918-715-187

US-09-918-715-232

US-10-301-822-199

US-10-408-765A-1873

US-10-474-794-187
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Sequence 621 App
Sequence 18, Appl
Sequence 187, Appl
Sequence 187, App
Sequence 199, App
Sequence 199, App
Sequence 1823, App
Sequence 187, App
Sequence 232, App
Sequence 232, App
Sequence 620, App
Sequence 621, Appl
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
773.5	786	786	786	786	786	903	1048	1058	1172	1299.5	1413	1478	1478	1483	1483	1493	1493	1493	1493	4	1499.5	1501	1501	1509	1509	1509	1509	1514	1514	1514	1514	1514	1514
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9	15	14	14	14	10	13	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	16	16	10	10	14	14	14	14	14	14
US-09-764-870-312	-10-104-047	-10-368-087-	-10-201-292-	-038-307-	-09-796-753-	-10-047-542-9	92-	-10-201-292-2	US-10-201-292-32	01-292-	-10-201-292-	US-10-201-292-12	07-	-292-	-307-1	US-10-201-292-16	-292-1	US-10-038-307-16	US-10-038-307-14	1-292-	-307-	US-10-201-292-26	US-10-038-307-26	4-794-3	-794-1	US-09-918-715-301		US-10-201-292-20	38-307-	92-	-10-038-30	-10-201-292-	US-10-038-307-2
312, Ap	e 263	e 16,	e 6,	equence	e 52,	e 99,	e 30,	e 28,	e 32,	æ	e 36,	e 12,	e 12,	e 10,	e 10,	16,	e 14,	e 16,	e 14,	O	e 22,	e 26,	e 26	е 30	e 19	e 30	e 19	e 20	e 20	e 24	Sequence 24, Appl	e 2,	Sequence 2, Appli

## ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-833-245-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 621, Application US/09833245 Publication No. US20040010134A1 GENERAL INFORMATION:
                                                                                                                              Query Match
Best Local Similarity
Matches 293; Conservat
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. SEQ ID NO 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PF546PCT
                      13
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RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGPERASEQIYYENRQGYRTASVIIA 120
                                                                               QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
                                                           QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                      0
                                                                                                                                      Score 1526; DB 11;
Pred. No. 1.1e-147;
; Mismatches 0;
                                                                                                                                                                           DB 11; Length
                                                                                                                                0;
                                                                                                                                      Indels
                                                                                                                                                                             403;
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                                                                                                                                      Gaps
                                                             87
                                                                                                 60
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US-10-474-794-232 US-09-833-245-620 US-09-796-753-12

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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KBEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Uddith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7863-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-18
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US-10-201-292-18
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US-10-038-307-18
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Sequence 18, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10038307
Publication No. US20030134786A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
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                                                                                                                                                                                                                                                                                                                                       241 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1526; DB 14;
100.0%; Pred. No. 1.8e-147;
htive 0; Mismatches 0;
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APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAT
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: U209/918,715
CURRENT APPLICATION NUMBER: 60/222,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/24,360
PRIOR APPLICATION NUMBER: 60/24,360
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for W
SEQ ID NO 18
LENGTH: 551
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASHSEQ for Windows Version
SEQ ID NO 187
LENGTH: 564
TYPE: PAT
ORGANIZM: Homo Bapiens
US-09-918-715-187
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US-09-918-715-187
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; ORGANISM: Homo
US-10-201-292-18
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Best Local Similarity
Matches 293; Conserv
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Publication No. US20030017157A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brad St. Croix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208
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                                                            61 RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120
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    LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA 180
                                                                                                                QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST 87
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                                    RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASBQIYYENRQGYRTASVIIA 147
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                                                                                                                                                                                             100.0%; Score 1526; DB 10;
100.0%; Pred. No. 1.9e-147;
ative 0; Mismatches 0;
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Pred. No. 1.8e-147;
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GENERAL INFORMATION:

APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
APPLICANT: Kenneth Kinzler
ITTLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 300-08-11
PRIOR FILING DATE: 300
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US-10-301-822-199
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US-09-918-715-232
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                                                                                                                                                                Sequence 199, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local
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APPLICANT: Millennium Pharmaceuticals, APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L. APPLICANT: Kamatkar, Shubhangi APPLICANT: Schlegel, Robert
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o. US20030148410A1
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Pred. No. 1.9e-147;
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Sequence 1823, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Tahy, Boin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088-465
CURRENT APPLICATION MUMBER: US/10/408,765A
CURRENT APPLICATION MUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID MOS: 3077
SOPTMARR: FBSELSEQ for Windows Version 4.0
SEQ ID NO 1823
LENGTH: 564
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: MCHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029PZRNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
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US-10-408-765A-1823
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
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                   ORGANISM: Homo sapiens
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es 293; Conserv
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US-10-474-794-187
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US-10-474-794-187
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOPTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelatein, Bert
APPLICANT: Kinzler, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.0%;
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268
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                     NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 293
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o. US20040213793A1
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Pred. No. 1.9e-147;
0; Mismatches 0;
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APPLICANT: KÜNTÜLET, KENNETH
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAT
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT APPLICATION NUMBER: 00/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILLING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILLING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 232
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR PPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 620
LENGTH: 403
TYPE: PRT
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US-09-833-245-620
Sequence 620, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
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US-10-474-794-232
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Best Local :
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                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
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o. US20040213793A1
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CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILLING DATE: 1998-10-30
PRIOR PELLING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILLING DATE: 1998-12-30
PRIOR FILLING DATE: 1998-12-30
PRIOR PILLING DATE: 1999-12-30
PRIOR PILLING DATE: 1999-12-30
PRIOR PILLING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILLING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/32,458
PRIOR APPLICATION NUMBER: 09/31,359
PRIOR APPLICATION NUMBER: 09/316,356
PRIOR APPLICATION NUMBER: 09/316,536
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR PILLING DATE: 1999-06-19
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR PILLING DATE: 1999-06-30
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US-09-796-753-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
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NAME/KEY: SITE
LOCATION: (368)
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NAME/KEY: SITE
LOCATION: (331)
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LOCATION: (320)
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Similarity 99.7%;
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Pred. No. 1.5e-146;
0; Mismatches 1;
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RESULT 12 US-10-038-307-2

Sequence 2, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
FILE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999

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; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12
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PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 12
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FILING DATE: 2000-09-20
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APPLICATION NUMBER: 09/
FILING DATE: 1999-12-29
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APPLICATION NUMBER: 09/474,071
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NEKPPSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCS
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CURRENT APPLICATION NUMBER: US/10/038,307; CURRENT FILING DATE: 2002-06-28; NUMBER OF SEQ ID NOS: 26; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; ELENGTH: 333; TYPE: PRT; ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                   APPLICANT: James B. ROTTMAN
APPLICANT: Thereag L.O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Cor
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo Sapiens
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US-10-201-292-2
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Publication No. US20030144193A1
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Best Local Similarity 100.0%; Pr
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                                                         LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA 180
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LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
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                                                                                                                                                                                                                                                99.2%; Score 1514; DB 14; 100.0%; Pred. No. 1.5e-146; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1514; DB 14; pred. No. 1.5e-146; 0; Mismatches 0;
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; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-24
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US-10-201-292-24
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                                                 GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/10038307 Publication No. US20030134786A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    Sequence 24, Application US/10201292
Publication No. US20030144193A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 291;
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Best Local Similarity
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APPLICANT: Theresa L. O'KERFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT EPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
RUMBER OF SEQ ID NOS: 26
LENGTH: 345
TYPE: PRT
ORGANISM: Homo
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Pred. No. 1.6e-146;
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US-10-201-292-24	-292-24
Query Match Best Local	/ Match 99.2%; Score 1514; DB 14; Length 345;
	vative 0; Mismatch
Ś	1 QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISDQLRMSFIVFST 60
Вb	28 QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST 87
Ş	61 RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120
90	88 RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGPERASEQIYYENRQGYRTASVIIA 147
Ş	121 LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQA 180
Вb	148 LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQA 207
Ş	181 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL 240
дb	208 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL 267
Ş	241 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCS 291
ДЬ	268 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCS 318
Search co	Search completed: June 13, 2005, 20:36:50 Job time : 94.9469 secs

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Copyright
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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OM protein - protein search, using sw model

June 13, 2005, 19:47:08; Search time 21.0213 Seconds (without alignments)
1341.095 Million cell updates/sec

Perfect score: Title:

Sequence: US-09-970-076-2\_COPY\_28\_320
1526
1 QGGRREDGGPACYGGFDLYF......DGLSFISSSVIITTTHCSDG

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Maximum Minimum DB seq length: 0
DB seq length: 2000000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	o.	U	4	w	N	_	NO	Result
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1018	917	817	698	559	597	460	574	747	567	493	500	1029	761	2944	764	496	929	3051	1888	1857	760	712	1747	724	1153	3124	1163	1153	Length	•
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collagen alpha 2(V	alph	kinesin-like prote	dnaK protein (heat	thrombospondin-rel	rop protein - frui	hypothetical prote		complement factor	cal prot	cartilage matrix p	cartilage matrix p	$\mathbf{-}$	complement factor		: factor	lag	Ë	hypothetical prote		collagen alpha 1(X	classical-compleme	immunodominant mic	collagen alpha 1(X	antigen Em100 - Bi	leukocyte surface	collagen alpha 1(X	cell surface glyco	9	Description	

45	44	43	42	41	40	39	38	37	36	35	34	<b>3</b> 3	32	31	30
92	92.5	93	94	94.5	95.5	95.5	95.5	96	96	96.5	97	97.5	98	98	98.5
6.0	6.1	6.1	6.2	6.2	6.3	6.3	6.3	6.3	6.3	6.3	6.4	6.4	6.4	6.4	6.5
292	642	340	843	1151	1179	932	334	689	272	676	3137	642	3176	741	537
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
B83736	B81917	E70121	A40970	A45226	A53213	JC5953	AF1166	F84811	A55348	T47637	A37797	H81185	CGHU3A	T46488	T04822
transposase (04) B	probable chaperone	hypothetical prote	undulin 1 - human	integrin alpha-1 c	integrin alpha-E c	inter-alpha-inhibi	transcription regu	probable retroelem	integrin alpha-1 -	hypothetical prote	collagen alpha 3(V	dnaK protein NMB05	collagen alpha 3(V	hypothetical prote	hypothetical prote

## ALIGNMENTS

cell surface glycoprotein CD11b precursor [validated] - human
Nalternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Ma
eukocyte integrin alpha (chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD

Reference number: A31108; MUID:88315033; PMID:2457584;

PID: 9307148

A;Accession: A31108
A;Molecule type: mRNA
A;Residues: 1-1153 <COR>
A;COB-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1;
A;COBE-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1;
A;COBE-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1;
A;Accession: A3108
A;Accession: A28915; MUID:88257215; PMID:2454931
A;Accession: A28915 adhesion receptor Mc

A;Molecule type: mRNA
A;Residues: 1-499,501-965,'P',967-1153 <ARN>
A;Residues: 1-499,501-965,'P',967-1153 <ARN>
A;Residues: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594'
A;Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594'
A;Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594'
A;Note: the authors translated the codon TAC for residue 1129 as Thr
A;Note: part of this sequence, including the amino end of the mature protein, was confirence.
A;Note: part of this sequence, including the amino end of the mature protein, was confirence.
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A;Note: part of the CDI.B; part of the mature protein, was confirence.
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A;Note: part of the CDI.B; part of the mature protein, was confirence.
A;Note: part of the CDI.B; part of the mature protein and the mature protein

A;Molecule type: DNA A;Residues: 1-9 <SHE>

A;Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215 R;Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G. Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988 A;Title: Molecular cloning of the alpha-subunit of human and guinea pig leuk A;Reference number: A94193; MUID:88190151; PMID:2833753

guinea pig leukocyte adhesic

A;Accession: A30892

A;Molecule type: mRNA A;Residues: 917-1042 <AR2>

A;Reference number: A32218; MUID:89098893; PMID:2563162 A;Accession: A32218 A;Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence receptor

A; Molecule type: mRNA A; Residues: 9-1153 <HIC>

A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

```
A,Map position: 16p11.2-16p11.2

A,Note: promoter contains a GATA motif and two Spl consensus binding sites
C,Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home
C,Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F,1-16/Domain: signal sequence #status predicted <SIG>
F,17-115/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F,17-1108/Domain: extracellular #status predicted <EXT>
F,148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F,148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F,146-433/Region: calcium/magnesium binding #status predicted
F,530-538/Region: calcium/magnesium binding #status predicted
F,533-601/Region: calcium/magnesium binding #status predicted <NMY>
F,1135-1135/Domain: transmembrane #status predicted <NMY>
F,166,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: granulocytes R;Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G. Blood 79, 865-870, 1992
A;Title: Characterization of the myeloid-specific CD11b promoter. A;Reference number: 152567; MUID:92144986; PMID:1346576
A;Accession: 152567
                                     RESULT
RWHU1C
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A;Note: the last three bases of intron 13, CAG, are included in some but not all matur A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
R;Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across A;Reference number: A30664; MUID:87076671; PMID:3539202
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A; Residues: 1-9 < RES>
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A; Residues: 1-499,501-1153 <FLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Fleming, J.
   cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219;Comment: A common beta chain (CD18) forms a heterodimer with this chain to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Status: translated from GB/EMBL/DDBJ
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Best Local :
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                                                                                                                                                                       315
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   glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 222
                                                                                                                                                                                                                                                                                                                                                                    DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR-----IADS--KDHVPP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                     FTFKEFQNNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT
                                                                                                                                                                                                                                                                                                      DGEKFGDPLGYEDVIPEADRE---GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ
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      CD11c
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26.2%; Pred. No. 0.0016;
tive 45; Mismatches 8
   precursor -
                                                                                                                                                                    IFAIEGTOTGSSSSFEHEMSOEGFSAA
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N;Alternate names: fibrochimerin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep_199 #Bequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
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                                                                                                                                     collagen alpha 1(XII) chain precursor -
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                                                                                                                                                                                                      RESULT
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A;Gene: GDB:ITGAX; CD11C
A;Gene: GD11C
A;Gene: GDB:ITGAX; CD11C
A;Gene: GD11C
A;Ge
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A;Molecule type: mRNA,
A;Residues: 1-755,'L',757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:YO0093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
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J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit, the leukocyta;Reference number: A35543; MUID:90153906; PMID:2303426
A;Accession: A35543
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A;Residues: 1-1163 <COR>
A;Cross-references: UNIPROT:P20702
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A; Contents: erratum
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J. Biol. Chem. 265, 12750-12751, 19
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A; Residues: 1-834 < CO2>
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FDALKDIQNQLKEK----IFAIEGTETTSSSSFELEMAQEGF
                                                                                       FOALQGIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF
                                                                                                                                                                                                                                                                                          LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 177
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A;Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C;Keywords: alternative splicing; cell binding; coiled coil; connective tissue F;1-23/Domain: signal sequence #status predicted <SIG> F;2-3/124/Product: collagen alpha 1(XII) chain #status predicted <MAT> F;24,1189-3124/Product: collagen alpha 1(XII) chain short splice form #status F;24-114/Domain: filt #status predicted <IIIA> F;24-114/Domain: fibronectin type III repeat homology <FN3A> F;317-301/Domain: von Willebrand factor type A repeat homology <VWA1> F;332-414/Domain: fibronectin type III repeat homology <FN3B> F;332-414/Domain: von Willebrand factor type A repeat homology <VWA2> F;332-414/Domain: fibronectin type III repeat homology <FN3C> F;629-1178/Domain: fibronectin type III repeat homology <FN3C> F;629-1178/Domain: fibronectin type III repeat homology <FN3C> F;612-895/Domain: fibronectin type III repeat homology <FN3C> Fibronectin type III repeat homology <FN3C> FN3C> F
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J. Biol. Chem. 262, 17724-17727, 1987
J. Riol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of A;Reference number: $22254; MUID:88087065; PMID:3121603
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A;Residues: 2960-2976, F', 2978-3074, 'AG' <GOR3>
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
R;Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified
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A; Molecule type: protein
A; Residues: 2772-2792; 886-2873 <GOR2>
R; Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
R; Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A; Title: Type XII collagen: distinct extracellular matrix
A; Reference number: A28037; MUID:87317590; PMID:3476925
A; Accession: A28037
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A;Residues: 1-3124 <YAM>
A;Cross-references: UniproT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:gA;Cross-references: UniproT:P1394; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:gA;Cross-references: UniproT:P1394; GB:D0082079; Pand der Rest, M.; Olsen, B.R.
R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A;Title: Type XII collagen. A large multidomain molecule with partial homology to A;Reference number: A34485; MUID:90082079; PMID:2584192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross_references: EMBL:X67327
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A,71tle: The two splice variants of collagen XII share a
A,Reference number: S28811; MUID:93042014; PMID:1420368
A,Accession: S28811
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A;Accession: S23814
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A;Residues: 2455-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:JO5137; NID:g211284; PIDN:AAA48635.1; PID:g211285
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                                                                                          F;995-1076/Domain: fibronectin type III repeat homology <FN3G>
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A; Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
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Willebrand
factor type A repeat homology
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F;2119-2199/Domain: fibronectin type III repeat homology <FN3P>
F;2217-2294/Domain: fibronectin type III repeat homology <FN3P>
F;2207-2294/Domain: fibronectin type III repeat homology <FN3P>
F;2207-2294/Domain: von Willebrand factor type A repeat homology <FW3R>
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F;2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status F;2509-2750/Domain: collagenous COL2 #status predicted <COL2>
F;2899-2901/Region: cell attachment (R-G-D) motif
F;2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
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F;3049-3124/Domain: non-collagenous NC2 #status predicted <NC1>
F;3
                                                                                                                                           A;Molecule type: DNA
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A;Residues: 1-11.53 cPYT>
A;Residues: 1-11.53 cPYT>
A;Residues: INIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Note: the authors translated the codon CAC for residue 569 as Gln
A;Note: the authors translated the codon CAC for residue 569 as Gln
R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept
A;Reference number: 159078; MUID:86287312; PMID:2942940
A;Accession: 159078
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F;1384-1465/Domain:
F;1474-1557/Domain:
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A;Title: Amino acid sequence of the murine Mac-1 alpha chain
A;Reference number: 800551; MUID:88312584; PMID:3044779
A;Accession: 800551
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                                    A;Residues:
                                                                     A; Molecule type: DNA
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F;1655-1738/Domain:
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;Species: Mus musculus (house mouse)
;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
;Accession: S00551; I59078
;Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
                                                                                                          ;Status: preliminary; translated
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fibronectin type III repeat homology <FN3I>
fibronectin type III repeat homology <FN3K>
fibronectin type III repeat homology <FN3IN-
fibronectin type III repeat homology <FN3N-
fibronectin type III repeat homology <FN3N-
fibronectin type III repeat homology <FN3N-
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Pred. No. 0.0097;
Promismatches 97;
                                                                                                                  from GB/EMBL/DDBJ
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A;Gene: Mac-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home C;Superfamily: cell adhesion; glycoprotein; transmembrane protein C;Keywords: cell adhesion; glycoprotein; transmembrane protein F;1-16/Domain: signal sequence #status predicted <SIG>
F;1-16/Domain: signal sequence #status predicted alpha chain #status experimental F;17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1106-1129/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
MOl. Blochem. Parasitol. 57, 1993
A;Title: Sequence of a major Eimeria maxima antigen homologous
A;Reference number: A48569; MUID:93149203; PMID:8426611
A;Accession: A48569
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A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F;238-296/Domain: thrombospondin type I repeat homology <THR1>
F;309-371/Domain: thrombospondin type I repeat homology <THR2>
F;372-432/Domain: thrombospondin type I repeat homology <THR3>
F;437-432/Domain: thrombospondin type I repeat homology <THR4>
F;431-493/Domain: thrombospondin type I repeat homology <THR5>
F;494-556/Domain: thrombospondin type I repeat homology <THR5>
F;494-556/Domain: thrombospondin type I repeat homology <THR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Eimeria maxima
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A48569
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A; Residues: 1-724 < PAS>
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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161
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                                            ELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP- 173
                                                                                                SDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDG
                                                                                                                                              TEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDG
                                                                                                                                                                                                  CTRLLDVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDL
                                                                                                                                                                                                                                            CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 122
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24.2%; Pred. No. 0.0038;
htive 50; Mismatches 96
                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                  Score 139; DB 2
Pred. No. 0.003;
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                                                                                                                                                                                                                                                                                                  Mismatches
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A;Molecule type: protein
A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime: F;40-204/Domain: von Willebrand factor type A repeat homology <FN3A>
F;236-317/Domain: fibronectin type III repeat homology <FN3B>
F;326-409/Domain: fibronectin type III repeat homology <FN3C>
F;418-498/Domain: fibronectin type III repeat homology <FN3D>
F;507-591/Domain: fibronectin type III repeat homology <FN3B>
F;507-591/Domain: fibronectin type III repeat homology <FN3B>
F;625-707/Domain: fibronectin type III repeat homology <FN3G>
F;625-707/Domain: fibronectin type III repeat homology <FN3G>
F;806-893/Domain: fibronectin type III repeat homology <FN3G>
F;924-1089/Domain: fibronectin type III repeat homology <FN3G>
F;924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
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R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
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A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
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C;Species: Gallus gallus (chicken)
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Eur. J. Biochem. 20
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A; Residues: 1472-1660 < APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A; Reference number: S30085
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A; Residues: 1-1747 < GER >
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A; Residues: 1472-1659 < GOR1 >
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;Accession: A45974; S30085; S22916; S217035; S20833
;Accession: A45974; S30085; S22916; S2017035; S20833
;Gerecke, D. R.; Folley, J. W.; Castegnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Line
Biol. Chem. 268, 12177-12184, 1993
                                                                                                                                                                                                                                                                                                                            ;1554-1659/Domain: triple helical domain COL1 #status
                                                                                                                                                                                                                                                                                                                                                      ;1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
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                                                                        DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGFDGTQVAIIQFSDDFRTEFKLNAYK 985
   DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 128
                                                                                                                             DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 70
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25.4%;
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5; Mismatches 114
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classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C2 (A)Alternate names: C3 convertase; C5 convertase; complement C2 (A)Specias: Mus musculus (house mouse) C1Date: 30-Sep-193 #sequence revision 30-Sep-1993 #text_change C1Date: 30-Sep-193 #sequence revision 30-Sep-1993 #text_change C1Accession: A38876; B36593; T54429 R1Bhlkawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R. submitted to GenBank, January 1991
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Mol. Blochem. Paraeltol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme A;Fttle: cnumber: A45638; MUID:92131064; PMID:1775171
A;Accession: A45638
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C;Species: Eimeria tenella
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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S31212
collagen alpha 1(XIV) chain
C;Species: Gallus gallus (ch
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F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-250/Product: complement C2b fragment #status predicted <C2B>
F;22-89/Domain: complement factor H repeat homology <FH12>
F;94-149/Domain: complement factor H repeat homology <FH2>
F;156-710/Domain: complement factor H repeat homology <FH3>
F;151-760/Product: complement C2a fragment long form #status predicted <C2A>
F;251-760/Product: complement C2a fragment short form #status predicted <C2A>
F;259-449/Domain: von Willebrand factor type A repeat homology <VFA>
F;259-449/Domain: typsin homology #status atypical <TRY>
F;478-747/Domain: typsin homology #status atypical <TRY>
F;478-747/Domain: typsin homology #status atypical <TRY>
F;27-62,49-89,94-136,122-149,156-197,182-210,470-530,499-515,593-609,647-674,685-715/Disu
F;27,117,297,340,474,478,663/Binding site: carbohydrate (Asn) (covalent) #status predicte
F;514,570,689/Active site: His, Asp, Ser #status predicted
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C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc
C;Keywords: alternative splicing; complement classical pathway; duplication; glycoproteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1; C;Complex: The proenzyme forms a complex with C4a and is activated by cleavage C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-760 < ISNA
A; Cross-references: EMBL: M57891; NID:g192436;
A; Cross-references: EMBL: M57891; NID:g192436;
R; Falus, A.; Wakeland, E.K.; McConnell, T.J.;
Immunogenetics 25, 290-298, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-760 <IS2>
A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1;
A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1;
R;Ishikawa, N.; Nonaka, M.; Wettel, R.A.; Colten, H.R.
J. Biol. Chem. 265, 19040-19046, 1990
A;Tittle: Murine complement C2 and factor B genomic and cDNA cloning reveals different me A;Reference number: A36593; MUID:91035430; PMID:2229060
A;Accession: B36593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 660-677, 'R', 679, 681-723, 'G', 725 <RES>
A;Cross_references: GB:M16271; NID:g199289; PIDN:AAA39562.1; PID:g199290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: cleaves complement C3 and complement C5 alpha chains
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A;Residues: 660-677,'R',679,681-723,'G',725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                   MND----GLSFISSSVII 285
                                                                                                                                                                                                                 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS
                                                                                                                                                                                                                                                                                                                                                        FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
                                                                                                                                                                                                                                                                                                                                                                                                                               KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DREQIROGLEELOKVLPGGDTYMHEGFERASEQIYYE-----NRQGYRTAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE 70
VGDPTSQHGKEFLVEDVII
                                                                                                                                      GNMSANASDQERTPWQVTFKPKSKETCQGS--LISDQWVLTAAHCFHDIQMEDHHLWRVN
                                                                                                                                                                                                                                                                                     LNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVSKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VIIALTDGELHEDLFFYSEREANRSRDLGAI-----VYCVGV------KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERSQ-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
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Pred. No. 0.014;
6; Mismatches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:AAA63294.1; PID:g192437
Gitlin, J.; Whitehead, A.S.;
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into C2a,
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ain precursor, (chicken)

short

form

chicken

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A;Residues: 1-1888 <TRUNA;Residues: 1-1888 <TRUNA;Cross-references: UNIPROT:P32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1; A;Cross-references: UNIPROT:P32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1; Baselchi, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Eur. J. Blochem. 212, 483-490; 1993

A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31211
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
$798476
$2798476
collagen alpha 1(XIV) chain precursor, long form - (C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998
C;Accession: $78476; $31211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, Eur. J. Blochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31212
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F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;543-614/Domain: fibronectin type III repeat homology <FN3C>
F;623-707/Domain: fibronectin type III repeat homology <FN3B>
F;623-708/Domain: fibronectin type III repeat homology <FN3F>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
F;923-1009/Domain: fibronectin type III repeat homology <FN3G>
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                                                                                                                                                                                                                                                                                                           A; Reference number: S78476
A; Accession: S78476
                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                        R, Trueb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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A;Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Ja:
                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: Coll4A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE
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larity 25.0%; Pred. No. 0.055;
Conservative 44; Mismatches 116; Indels 2
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C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; F;1-28/Domain: signal sequence #status predicted <SIG>F;29-188/Product: collagen alpha I(XIV) chain, long form #status predicted <MAT>F;29-110/Domain: fibronectin type III repeat homology <FN3A>F;156-320/Domain: fibronectin type III repeat homology <FN3B>F;156-320/Domain: fibronectin type III repeat homology <FN3B>F;442-525/Domain: fibronectin type III repeat homology <FN3B>F;442-525/Domain: fibronectin type III repeat homology <FN3B>F;441-525/Domain: fibronectin type III repeat homology <FN3B>F;623-707/Domain: fibronectin type III repeat homology <FN3B>F;623-707/Domain: fibronectin type III repeat homology <FN3B>F;623-707/Domain: fibronectin type III repeat homology <FN3B>F;623-109/Domain: fibronectin type III repeat homology <FN3B>F;922-1009/Domain: fibronectin type III repeat homology <FN3B-P;922-1009/Domain: fibronectin type III re
                                                                                                                                                                                                                                                                                                                                                                                                                  F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1>F;754-793/Domain: fibronectin type II repeat homology <2F1>F;1201-1244/Domain: EGF homology <EGF>
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C;Genetics:
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A; Residues: 1-3051 <SMI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Caenorhabditis elegans;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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ELFEIGRSKTRVGLIQYSDQIRHEFDLDQYGDRDSLLKGISETQ-YLTGLTRTGAAIQHM
                                                                 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                                                   CYGGFVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVFKNEVLRFVREFV
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                                                                                                                                                                                                                                                                              8.4%; Score 128; DB
27.1%; Pred. No. 0.15;
tive 31; Mismatches
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A;Molecule type: mRNA
A;Residues: 157-290,'L', 292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666;
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                                                                                                                                                                                                                                                                                      Cartilage matrix protein precursor - human C;Species: Homo sapiens (man) C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 C;Accession: A37979; B37979
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A;Title: Monoclonal antibody MT2 identifies the urodele A;Reference number: I51027; MUID:95246925; PMID:7729585
A;Accession: I51027
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                                                                                                      A;Residues: 1-496 <JEN>
A;Cross-references: UNIPROT:P21941; GB:J05667
                                                                                                                                                                        A;Reference number: A37979;
A;Accession: A37979
                                                                                                                                                                                                                   J. Biol. Chem. 265, 19624-19631, A,Title: Structure and chromosom
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                                                                                A, Accession: B37979
                                                                                                                                              A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQEGF-----TGPADSARKLSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EGFERASEQIYYENROGYR-----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QEVYVRGTQTTTVLVGLKPETEYYVN
                                                                                                                                                                                                                                                              Osborne-Lawrence, S.L.; Sinclair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                              chromosomal location of the human gene encoding cartilage matrix
7979; MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.7%; Score 118; DB 2; Length 929; 21.2%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
           GB:J05667; NID:g180651; PIDN:AAA63904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273
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                                                                                                                                                                                                                                                              A.K.;
                                                                                                                                                                                                                                                                                                         #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                Jr., R.L.; Byers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain
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           PID:
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A;Molecule type: mRNA
A;Residues: 467-546;550-595;752-764 <MOO>
A;Residues: 467-546;550-595;752-764 <MOO>
A;Cross-references: GB:J00185; GB:J00186
A;Note: the authors translated the codon TAC at 519 as Thr; t
A;Nole; J.B.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
J. Biol. Chem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human
A;Reference number: A20751; MUID:84161997; PMID:6546754
A;Accession: A00934
R;Christie, D.L.; Gagnon, J. Biochem. J. 209, 61-70, 1983
                                                   A; Note: glycosylation sites were
                                                                                    A;Note: nucleic acid translation differs from A;Note: 736-Ser was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN:CAA51389.1; R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R. Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein factor B, a A;Reference number: A44622; MUID:83039428; PMID:6957884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-496/Product: cartilage matrix protein #status predicted <MAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWA1>
F;227-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;76,344/Binding site: carbohydrate (Asm) (covalent) #status predicted
                                                                                                                                                                      A; Molecule type: protein; mRNA
A; Residues: 26-764 < MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S34075
A; Accession: S34075
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                                                                                                                                              A;Cross-references: GB:K01566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A44622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-764 < MEJ >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Mejia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement factor B precursor [validated] - human
N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-l
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: cartilage matrix protein; EGF homology; von
C;Keywords: glycoprotein; homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:127280; OMIM:115437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
;Species: Homo sapiens (man)
;Date: 19-Feb-1984 #sequence revision 05-Aug-1994 #text change 09-Jul-2004
;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339
;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;76,344/Binding site: carbohydrate (Asn) (covalent) #status;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  госат
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 CYGG-----FDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMSFIV---FSTR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----YENRQGYRTAS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTAD-FKTINQIGKKLQKKICVE---EDP---CACESLVKFQAKVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKVGIVFTDGRSQD----YINDAAKKAKDLGFKMFAVGVGNAVEDELREIASEPVAEHYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS--KDHVF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSGGGGSSATDLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQVGLVQYSSSVR 324
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Pred. No. 0.21
35; Mismatches
                                                         determined
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                                                                                                                                                                                                                                                                                                                                                                             nucleic acid translation
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                                                                                                               ä
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                                                                                                               300-Leu,
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Amino acid sequence

of the

В

fragment

from complement

factor B.

Sequence

of the

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A; Welcule type: mRNA
A; Residues: 16-225; F', 227-259 < MOR>
A; Residues: 16-225; F', 227-259 < MOR>
A; Residues: 16-225; F', 227-259 < MOR>
R; Schwaeble, W.; Luttig, B.; Sokolowski, T.; Es
Immunobiology 188, 221-232, 1993
A; Title: Human complement factor B: functional
A; Title: Human complement factor B: functional
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A; Residues: 339-509 <All>
A; Residues: 339-509 <All>
A; Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1;
A; Cross-references: GB:J00126; N.D.
Cell 48, 331-342, 1987
A; Title: Cell-specific expression of the human complement pro
A; Reference number: A25971; MUID:87102880; PMID:3643061
A; Accession: B25971
                                                                                              A;Map position: 6p21.3-6p21.3
A;Map position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3;
A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 270-329 <NIB>
A;Residues: 270-329 <NIB>
A;Residues: 120-329 <NIB>
A;Rote: binding site for carbohydrate to lysine under artificial conditions
R;Morley, B.J.; Campbell, R.D.
R;Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
A;Title: Internal homologies of the Ba fragment from human complement component
A;Reference number: A44628; MUID:84158524; PMID:6323161
A;Recession: A44628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689
R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.
Mol. Immunol. 30, 1587-1592, 1993
A;Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic A;Reference number: 157824; MUID:94067177; PMID:8247029
A;Accession: 157824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Campbell, R.D.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene A;Reference number: A19947; MUID:83273641; PMID:6308626
A;Accession: A19947
  A; Pathway:
                                                           A;Description: Bb is a serine proteinase;
                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-31,'Q',33-764 <RE2>
A;Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1;
C;Comment: 292-Cys has a free sulfhydryl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-764 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: I54409; A; Accession: I54409
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A; Accession: S14339
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Biochem. J. 274, 473-480, 1991
A;Title: The principal site of glycation of human complement
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A;Residues: 346-764 <CAM>
A;Crose-references: GB:J00125
A;Accession: B19947
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                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:119726; OMIM:138470
                                                                                                                                                                                                                                                                                                                A;Gene: GDB:BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-99 <WUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 260-296,'T'
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                                                                                                                                                                                                                                                                                                                                                Genetics:
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pathway
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                                                           C3/C5
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PMID:8225386
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                                                           convertase cleaves
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F;26-764/Product: complement factor B #status experimental <MAT>
F;26-764/Product: complement factor Ba fragment #status experimental <BAF>
F;37-98/Domain: complement factor Ba fragment #status experimental <BAF>
F;103-158/Domain: complement factor H repeat homology <FH1>
F;103-158/Domain: complement factor H repeat homology <FH3>
F;105-218/Domain: complement factor H repeat homology <FH3>
F;106-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF>
F;260-764/Domain: von Willebrand factor type A repeat homology <VFA>
F;482-752/Domain: trypsin homology #status atypical <TRY>
F;482-752/Domain: trypsin homology #status atypical <TRY>
F;482-752/Domain: trypsin homology #status atypical <TRY>
F;37-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Dif
F;122,142,285,378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
F;526,576,699/Active site: His, Asp, Ser #status experimental
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A54849
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A;Residues: 1-2944 <CHR>
A;Residues: 1-2944 <CHR>
A;Residues: 1-2944 <CHR>
A;Cross-references: UNIPROT:Q02388; GB:L02870; NID:g987124;
B;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A;Title: Molecular cloning and characterization of type VII
A;Reference number: PH0844; MUID:92231902; PMID:1567409
A;Accession: PH0844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text change 09-Jul-2004 C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686 R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J. J. Biol. Chem. 269, 20256-20262, 1994 A;Title: Cloning of human type VII collagen. Complete primary sequence of the A;Reference number: A54849; MUID:94327588; PMID:8051117
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C;Keywords: acute phase; complement alternate pathway;
F;1-55/Domain: signal sequence #status predicted csICs
F;1-55/Domain: signal sequence #status predicted csICs
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Baue Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
                                                                                                           A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 'EPR',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C',
A;Croos-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699
A;Experimental source: keratinocyte
A;Experimental source: keratinocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: not compared with conceptual translation
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Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrola
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19.6%; Pred. No. 0.37;
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F;36-201/Domain: von Willebrand factor type A repeat homology <FN1>F;231-318/Domain: fibronectin type III repeat homology <FN1>F;231-413/Domain: fibronectin type III repeat homology <FN1>F;327-413/Domain: fibronectin type III repeat homology <FN2>F;414-502/Domain: fibronectin type III repeat homology <FN3>F;508-593/Domain: fibronectin type III repeat homology <FN4>F;508-693/Domain: fibronectin type III repeat homology <FN4>F;508-693/Domain: fibronectin type III repeat homology <FN5>F;686-771/Domain: fibronectin type III repeat homology <FN7>F;776-862/Domain: fibronectin type III repeat homology <FN8>F;954-045/Domain: fibronectin type III repeat homology <FN8>F;954-1045/Domain: fibronectin type III repeat homology <FN9>F;1052-1219/Domain: fibronectin type III repeat homology <FN9>F;1170-1172/Region: cell attachment (R-G-D) motif F;1189-1253/Region: cell attachment (R-G-D) motif F;1254-2784/Region: cell attachment (R-G-D) motif F;2553-2555/Region: cell attachment (R-G-D) motif F;2553
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R;Christiano, A.M.; Ryymaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly ---> Ser sul A;Reference number: A55255; MUID:94224777; PMID:8170945
A;Contents: annotation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit cannot subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;17-2944/Product: collagen alph F;17-1253/Domain: amino-terminal F;36-201/Domain: von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: structural component of extracellular polymer C; Keywords: coiled coil; extracellular matrix; glycoprotein; F;1-16/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A/Map position: 3p21.3-3p21.3
A/Note: defects in this gene (
A/Note: there are 118 introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 2, 273-278, 1993
A;Title: The carboxyl-terminal half of type
A;Reference number: I48103; MUID:93271985; P
A;Accession: I84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 815-892,'E',894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
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A;Accession: S16316
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J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles mu
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A; Residues: 2395-2871, '8', 2873-2944 <RE2>
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NyResidues: 'EPR',372-517,'DV',520-540,'W',542-1255 <RES>
NYResidues: 'EPR',372-517,'DV',520-540,'W',542-1255 <RES>
NYRESIDUES: 'EPR',372-517,'DV',520-540,'W',542-1255 <RES>
NYRESIDUES: 'GRANGE GRANGE GRA
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;Cross-references: GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
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;Residues: 'A', 1240-1246,'G', 1248-1250,'XE', 1253-1255,'Q', 1257,'E';2032,'C',2034-2041;
;Rots: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number: 156328; MUID:93107742;
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                                                                carboxyl-terminal nonhelical #status predicted <NC2>
animal Kunitz-type proteinase inhibitor homology <BPI>
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Best Local Similarity
210
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                                                                                                            129
                                    187 SILKKSCI------EILAAEPST 203
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LVSRRVCTTAGGVPVTRPPDDSTSAPRDLVLSEPSS
                                                                                                           DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH 186
                                                                                                                                                 GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                   TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE 128
                                                                                                                                                                                                                        DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAOGVRFATVOYSDDPRTEFGLDAL
                                                                                                                                                                                                                                                            DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
                                                                        DLV---DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVND-FSILRTLLP 209
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                                                                                                                                                                                                                                                                                                                                                                     bonds: interchain #status predicted
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Search completed: June 13, Job time : 21.0213 secs 2005, 20:06:35



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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Q28984
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Q8T5C3
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TAM HUMAN
Q8T5C7
TAM MOUSE
C015C HUMAN
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C02 MOUSE
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Q9h6x2 homo sapien
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                                                                                                                                                                                                                                                                                      5 homo sapien
2 mus musculu
2 mus musculu
6 homo sapien
7 rattus norv
9 homo sapien
8 halocynthia
1 homo sapien
5 myrilus edu
3 myrilus edu
3 myrilus gal
2 homo sapien
2 mytilus gal
2 homo sapien
4 gallus gal
5 mus musculu
8 eimeria max
7 mus musculu
                                                                   1 eimeria ten
0 mus musculu
9 neospora ca
3 homo sapien
0 mus musculu
5 homo sapien
4 sus scrofa
4 gallus gall
9 mus musculu
7 mus musculu
2 caenorhabdi
5 caenorhabdi
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		; Crea	02; Q9NVP3; (Rel. 41. Created)	Q9H6X2; Q96P02; 28-FEB-2003 (Re	មក
	PRT; 564 AA.	D;	STANDARD;	HUMAN ATR1_HUMAN	133
				ļ.	RESULT 1
	ALIGNMENTS				
Q9p218 homo sapien	KF10_HUMAN	9	7.7 132	117.5	4.
Q6pi59 homo sapien	2 Q6P159	4 2	7.7 1284	117.5	44
Q8ivx1 homo sapien	2 Q8IVX1	7 2	7.7 637	117.5	4.
Q91145 notophthalm	CA1C NOTVI		7.7 929	118	4.
Q95li2 bos taurus	_				4.
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Q75r52 lymnaea sta	_	9 2	7.8 919	118.5	<u>س</u>
Q8c720 mus musculu	? Q8C720				ω
Q8cbt2 mus musculu	_		7.8 44	118.5	بى
Q6dcq6 xenopus lae				120.5	ω
Q7rf52 plasmodium			7.9 2401		ω
Q8cip8 rattus norv					ų
Q6mg73 rattus norv	2 Q6MG73		7.9 758	121	w
Q9ji30 rattus norv	2 Q9JI30	1 2	8.1 115	123	ω

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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishiqaki H., Watanabe T., Suqiyama A., Takemoto M., Kawakami B.,	Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,	Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,	Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,	Kusano J., Kanehori K., Takahashi-Puiii A., Hara H., Tanase TO.,	Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,	Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,	A Naganari K., Murakami K., Yasuda T., Iwayanagi T., wagatsuma M., A Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,	Yamamoto JI., Saito K., Kawai Y., Isono Y., Nakamura Y.,	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,	Wakamatsu A. Hayashi K. Sato H. Nagai K. Kimura K. Makita H.	PubMed=14702039; DOI=10.1038/ng1285;	SEQUENCE OF 184-364 FROM N.A. (ISCHORM I), AND SEQUENCE FROM N.A. (ISCHORM I).		Nature 414:225-229(2001).	"Identification of the cellular receptor for anthrax toxin.":	MEDLINE=21557240; PubMed=11700562; DOI=10.1038/n35101998;	SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH ANTHRAX TOXIN.	[2]	"Genes expressed in human tumor endothelium.";		Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,	St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,	MEDITURE 204074666 DITURE 110047088 DOTING 1126/8510106 280 5482 1107.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Rutheria: Primates: Catarrhini: Hominidae: Homo		Name=ANTXR1; Synonyms=ATR, TEM8;	2004 (Rel. 44, Last annotation update)	2003 (Rel. 41, Last	28-FRR-2003 (Rel 41 (Treated)	ATR1_HU	RESULT 1

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RX MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RX Hausner R.D., Collins F.S., Wagner L., Shenefer C.F., Bhat N.K.,
RX Hausner R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RX Hausner R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Hausner R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Rahas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
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RX Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,
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RX Pathey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Rahey J., Helton E., Ketteman M., Marcan B.D., Dickson M.C.,
RX Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RX Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
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RX Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RX Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RX Generation and initial analysis of more than 15,000 
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                                               This
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"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100;
Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.;
"Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH ANTHRAX TOXIN
                                                                                           TISSUE SPECIFICITY: Highly expressed in tun
but not in normal endothelial cells.
DOWAIN: Binding to PA seems to be effected
SIMILARITY: Belongs to the ATR family.
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Cellular role is not yet known.
SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis. Binding does not occur in the presence of calcisuBCELLULAR LOCATION: Type I membrane protein (Probable).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event-Alternative splicing; Named isoforms=4; Comment=Experimental confirmation may be la
                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low levels due to a premature codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                           IBOId=Q9H6X2-3;
                                                                                                                                                                                                                                                                                                                               IsoId=Q9H6X2-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isoforms;
                                                                                                                                                                                                                            IsoId=Q9H6X2-4; Sequence=VSP_000448,
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Bioinformatics
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InterPro; IPR008399; Ant_C.
InterPro; IPR002035; VWF_A.
Pfam; PF05587; Anth_Ig; I.
Pfam; PF05586; Ant_C; 1.
Pfam; PF00092; VWA; 1.
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:21014; ANTX
H-InvDB; HIX0002125; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                         181
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                                                                                                121
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BC012074; AAH12074.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF279145;
                                                                                                                                                                                                  293;
                                                                                                                   88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:21014; ANTXR1.
                                                                                                                                                                                                            Similarity
                                                                                                                                                                       QGGRREDGGPACYGGFDLYFILDXSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
           NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
                                                 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
                                                                                        LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQA
                                                                                                                                 RGTTLMKLTEDREQIRQGLEEI
NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
                                      LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
                                                                              LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA
                                                                                                                   RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA
                                                                                                                                                           QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
                                                                                                                                                                                                                                         564
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                                                                                                                                                                                                                                                                                                                                                             369
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                           319
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BAB15128.1;
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                                                                                                                                                                                                          100.0%;
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ALT_FRAME.
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                                                                                                                                                                                                                                                                                                                                                                                                              Pro-rich.
N-linked
                                                                                                                                                                                                 Score 1526;
Pred. No. 3.3
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Anthrax toxin receptor 1.
Extracellular (Potential).
                                                                                                                                                                                                                                        /FTId=VSP 000448.
Missing (In isoform 4).
/FTId=VSP 000449.
B118A00ADSDF2233 CRC6.
                                                                                                                                                                                                                                                                                                                                Missing (in isoform 2).
/FIId=VSP_000445.
NEKEPESVEDTYLLCPAPILKEVGMKAALOV
WVSSTSGFKEGNSHPCLPARPHT (in iso
                                                                                                                                                                                                                                                                                         /FTId=VSP_000447.
DGSILAIALLILFLL -
                                                                                                                                                                                                                                                                                                            Missing
                                                                                                                                                                                                                                                                                                                                                                                          N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Asp/Glu-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
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Missing (in isoform 2)
                                                                                                                                LQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA
                                                                                                                                                                                                                                                                                                                                                                                nked (GlcNAc...) (Potential)
nked (GlcNAc...) (Potential)
nked (GlcNAc...) (Potential)
-> NKIK (in isoform 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (highly acidic).
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                                                                                                                                                                                                                                                                                           -> LHKIASGPTTAACME
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                                                                                                                                                                                                                      564;
                                                                                                                                                                                                                                                                                                                                 isoform
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                    293
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Q9CZ52;
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, L
05-JUL-2004 (Rel. 44, L
Anthrax toxin receptor
                                This
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Antxr1; Synonyms=Atr,
Mus musculus (Mouse).
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                                                                                       SIMILARITY: Belongs to the ATR family. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative
                                SWISS-PROT entry is copyright.
                                                                                                                                                       IsoId-09CZ52-2; Sequence=VSP_000450; Note=No experimental confirmation available; MAIN: Binding to PA seems to be effected thr by similarity).
                                                                                                                                                                                                                                                                                                              IsoId=Q9CZ52-1;
   the
   SW188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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   Institute
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Bioinformatics and the EMBL
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                             a collaboration
outstation
                                                                                                                                                                                    domain
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Name=ANTXR2; Synonyms=CMG2; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

morphogenesis

protein-2)

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InterPro; IPRO08400; Anth Ig.
InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PF05587; Anth Ig; I.
Pfam; PF05586; Ant C; 1.
Pfam; PF00992; VWA; 1.
                                                                 ATR2 HUMAN STANDARU;
ATR2 HUMAN STANDARU;
P58335; Q86UI1; Q8NB13; Q96NC7;
P58325; Q86UI1; Q8NB13; Q96NC7;
P58325; Q86U11; Q8NB13; Q96NC7;
P582325; Q86U11; Q8NB13; Q96NC7;
P582325; Q86U11; Q8NB13; Q96NC7;
P582325; Q86U11; Q96NC7; Q96NC7;
P582325; Q86U11; Q96NC7; Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF378762; AAL11999.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                     QGIIHSILKKSCIBILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTLMKLTEDREQIRQGLEBLQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIAL
                                                                                                                                                                                                                                                                                      EKPFAVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.9%;
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Pred. No. 7.
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RA PLUMEGUSIA (U.S.) (DLSI) (U.S.) (DLSI) (U.S.) (DEUKI T., Sugiyama T., Irie R., RA Ota T., Suzuki Y., Nishikawa T., Otawai T., Sugiyama T., Irie R., RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Tanaka T., Tanaka T., Tanaka T., Tanaka T., Tanaka T., Ishii S., RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Ra Tanikawa Y., Abe K., Kamihara M., Watanabe M., Hiraoka S., Chiba Y., Ishibashi T., Yamashita H., Murakawa K., Rujimori K., Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Ra Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Ra Tanase T.-O., Ra Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Antsuka S., Chiba Y., Takahashi Fujii A., Hara H., Tanase T.-O., Ra Nomiya S., Moniyama H., Satoh N., Takama S., Forsida M., Hotuta T., Suosida N., Hotuta T., Suzuki O., Ra Nomiya S., Moniyama H., Satoh N., Takama S., Fokuzumi Y., Suzuki O., Ra Moriya S., Moniyama H., Satoh N., Takama S., Fokuzumi Y., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Takima Y., Okamoto S., Ra Numira R., Wakami T., Nobutake N., Itakura S., Fukuzumi Y., Ra Pujimori Y., Kobatake N., Itakura S., Fukuzumi Y., Okamoto S., Ra Numira R., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Pujiwara T., Satoh T., Shirai Y., Sasaki M., Sasaki M., Nasuho Y., Yamashita R., Nakajima Y., Matanabe M., Komatsu T., Nakagawa K., Ra Nukira R., Nakajima Y., Matanabe M., Kukuchi H., Masuho Y., Yamashita R., Ra Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Makagawa K., Sanaki M., Masuho Y., Yamashita R., Kawabata T., Satoh T., Shirai Y., Nakagawa K., Makagawa K., Makajima Y., Matanabe M., Mat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.A., Davis G.E.; Maxwell S.A., Davis G.E.; "Differential gene expression during capillary morphogenesis collagen matrices: regulated expression of genes involved in membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling."; J. Cell Sci. 114:2755-2773 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Synovial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 78-489 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scobie H.M., Rainey G.J.A., Bradley K.A., "Human capillary morphogenesis protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100;
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MEDLINE=21539596; PubMed=11683410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION
                                                                                                                                                                                    following preference: calcium > manganese > magnesium > zinc.
Seems to bind to collagen type IV and laminin.
SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmic reticulum and not at the plasma membrane.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                         . Genet. 36:40-45(2004).
FUNCTION: Cellular role is not yet known.
SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the
                                                                                                                                                                   Event=Alternative
                        IsoId=P58335-3;
Note=No
                                                                       IsoId=P58335-2;
                                                                                                                    [soId=P58335-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ع
Sequence=VSP_008344, VSP_008345;
ental confirmation available;
                                                                  Sequence=VSP_008343;
                                                                                                                 Sequence=Displayed;
                                                                                                                                                                splicing;
                                                                                                                                                                   Named isoforms=4;
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CARBOHYD
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Pfam;
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EMBL; AK091721;
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                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:21732; ANTXR2
MIM; 608041; -.
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InterPro; IPR002035; VWF_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P58335-4; Sequence-VSP_008346;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in colon, heart,
liver, peripheral blood leukocytes, placenta, i
small intestine and spleen.
DOMAIN: Binding to PA seems to be effected thre
SIMILARITY: Belongs to the ATR family.
SIMILARITY: Contains 1 VWFA domain.
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                                                                     155
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                                                                                                                                                                                                                      Similarity
                                                                                                                GDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQI--QKAGGLKTSSIIIALTDGKLDGL
                                                                                                                            EDREQIRQGLEELQKYLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHED
                                                                                                                                                                          PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLT
 TYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDG
                      AQSCTEILELQPSSVCVGEEFQIVLSGRGFMLGSRNGSVLCTYTVNETYTTSVKPVSVQL
                                         KKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVED
                                                                     VPSYAEKEAKISRSLGASVYCVGVLDFEQAQLERIADSKEQVFPVKGGFQALKGIINSIL
                                                                               LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
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489 AA;
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BAB70976.1; ALT_INIT.
BAC03731.1; -.
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                                                                                                                                                                                                          Score 786; DB
Pred. No. 9.6e
54; Mismatches
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FTICHVSP 008343.

TLDVSVSFNGEKSVLTSGSLIVTATECSNGIAAI -> WGLT
TLDVSVSFNGEKSVLTGGSGDPPTSAS (in isoform
                                                                                                                                                                                                                                                                                                               Missing (In isofo /FTId=VSP_008345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
Anthrax toxin receptor 2.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                         N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be effected through the VWA domain.
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.6e-54;
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centa, skeletal
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Witrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altechul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Hillalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pahey J., Helton E., Ketteman M., Wadan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                    EMBL; BC076595; AAH76595.1; -. GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00104872; F:receptor activity; IEA.
InterPro; IPR008400; Anth Ig.
InterPro; IPR008399; Ant_C.
InterPro; IPR008399; Ant_C.
InterPro; IPR008399; Ant_C.
Pfam; PP05887; Anth Ig; I.
Pfam; PP05886; Ant_C; 1.
Pfam; PP05886; Ant_C; 1.
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Eukaryota; Metazos; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                            SMART; SM00327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.; "Generation and initial analysis
                                                                                                                                                                                                                                                                      PROSITE; PS50234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                                                                                                                                                                                     Similarity
                                 GDRYKIGKGLEDLKAVKPVGETYIHEGLKLANEQI--QNAGGLKASSIIIALTDGKLDGL
                                                                                                 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                      EDREQIRQGLEBLQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequences."
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Last sequence update)
Last annotation update)
                                                                                                                                                                                     Score 770; DB 2;
Pred. No. 1.8e-52;
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sequencing Genome Res. [6]
                                                                                                                 STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913, PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshika M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yoneda Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

"RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Sugahaziaki Y., Konno H., Okazaki Y., Muramatsu M., Shibata Konno H., Okazaki Y., Muramatsu G., Shibata Konno H., Okazaki Y., Muramatsu G., Sugahara Y., Shibata Y., Sugahara Y., Sugahara Y., Shibata Y., Shibata Y., Shibata Y., Sugahara Y., Shibata                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome b
60,770 full-length cDNAs.";
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MEDLINE=99279253; PubMed=10349636;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical Proline-rich regi
Willebrand factor type A domain containing protein, full insert
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Q8BVM2;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria;
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                                                   pipeline with 384 multicapillary sequencer.";
. 10:1757-1771(2000).
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Sciurognathi;
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STRAIN-C57BL/6J; TISSUB-Testis;

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Ahadachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Ahayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Ahayashida K., Hayatsu N., Hiramoto K., Kagawa I., Kasukawa T.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nomura K.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nomura K.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koya S.,

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Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koya S.,

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Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Kojima Y., Kondo S., Konno H., Kojima Y., Kojima Y., Kondo S., Konno H., Kojima Y., Kondo S., Konno H., Kojima Y., Kondo S., K
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Q96EC6;
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SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausmer R.D., Collins F.S., Wagner I., Sheamen C.M., Schuler G.D.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                               TISSUE=Breast;
MEDLINE=22388257;
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTXR1 protein Name=ANTXR1;
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                                                                                                                                                                       PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
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42.2%; Pred. No. 2.3e-39;
tive 58; Mismatches 105;
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Catarrhini; Hominidae; Homo
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"Cloning of rat alpha D, a novel beta 2 integrin.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atheroselerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood (By similarity).

1. SUBUNIT: Heteorodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

1. SUBCELIULAR LOCATION: Type I membrane protein (By similarity).

1. DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrir with I-domains do not undergo protease cleavage.

1. SIMILARITY: Belongs to the integrin alpha chain family.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008400; Anth_Ig.
                                                                                                                                                                                                               STRAIN-Sprague-Dawley;
O'Brien M.M., VanderVi
Gallatin W.M.;
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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05-JUL-2004 (Rel. 44, Last sequence up
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c. Natl. Acad. Sci. U.S.A.
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Rodentia;
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95.1%;
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Calcium; Cell adhesion; Glycoprot.
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Pfam; PF00357; Integrin_alpha;
Pfam; PF00092; VWA; 1.
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InterPro; IPR002035; VWF_A.
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1 VWFA domain.
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Cytoplasmic (Potential).
FG-GAP 1.
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FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
Potential.
Potential.
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MBL outstation -
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RESULT 8
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Q13349; Q15575; Q15576;
16-OCT-2001 (Rel. 40, Create:
16-OCT-2001 (Rel. 40, Last s:
05-JUL-2004 (Rel. 44, Last a:
Integrin_alpha-D_precursor ()
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INTERACTION WITH VCAM1.
INTERACTION WITH VCAM1.
MEDLINE=99059842; PubMed=9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gall
Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and fi
"alphadbeta2 integrin is expressed on the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o
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J. Immunol. 163:1984-1990(1999).
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Eukaryota; Metazoa;
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MEDLINE=99370002; PubMed=10438935;
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J. Biol. Chem. 275:8959-8969(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 171:291-294(1996).
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=ITGAD;
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FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood.

SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUB SPECIFICITY: Expressed moderately on myelomonocytic cell lines and subsets of peripheral blood leukocytes and strongly on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2-integrin alpha subunit.";
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Catarrhini; Hominidae;
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EMBL; U40277; AAB60637.1; -.
EMBL; U40277; AAB60638.1; -.
EMBL; U40279; AAB60638.1; -.
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InterPro; IPR002035; VWF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5
SMART; SM00327; VWA; 1.
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PROSITE; PS50234; VWFA; 1.
Calcium; Cell_adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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atherosclerotic plaques, and on splenic red pulp macrophages.
DOMAIN: The integrin I-domain (insert) is a VWFA domain. Inte
with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
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Cytoplasmic (Potential).

FG-GAP 1.

FG-GAP 2.

WWPA.

FG-GAP 3.

FG-GAP 6.

FG-GAP 6.

FG-GAP 7.

Potential.

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Best Local
                                                                                              J. Immunol. 166:1710-1713(2001).

-|- SUBCELULAR LOCATION: Type I membrane
-|- SIMILARITY: Belongs to the integrin al.
EMBL; AB048261, BAB21479-1;
-- HSSP; P11215; 1BHQ.
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0008305; C:integral to membrane; IEA.
GO; GO:0005515; F:protesin binding; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IE
GO; GO:0007129; P:integrin-mediated signal
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.

Pfam, PF00192; VWA; 1.
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01-JUN-2001 (TrEMBLrel. 17, I
01-JUN-2003 (TrEMBLrel. 24, I
Integrin alpha Hrl precursor.
PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int alpha; 1:
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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NCBI_TaxID=7729;
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MEDLINE=21103187; PubMed=11160215;
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yota; Metazoa; Chordata; Urochordata; Ascidiacea;
dobranchia; Pyuridae; Halocynthia.
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GHPW -> ATP (in Ref. 2).
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V -> A (in Ref. 2).
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Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                              Genew; HGNC:22989; COL22A1.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005138; F:structural molecule activity; IE.

GO; GO:0007155; F:cell adhesion; IEA.

GO; GO:0007155; F:cell adhesion; IEA.

GO; GO:0006817; P:phosphate transport; IEA.

InterPro; IPR008161; Clighelix.

InterPro; IPR008161; Collagen.

InterPro; IPR008169; ConA like_lec_gl.

InterPro; IPR003129; TSP N.

InterPro; IPR003129; TSP N.

InterPro; IPR003035; VWP_A.

Pfam; PF01391; Collagen; 16.

Pfam; PF01391; Collagen; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
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SIGNAL 1
CHAIN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8NFW1
                                                                                               PROSITE;
Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1 type XXII collagen.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koch M., Jin W., Ashworth T.,
Submitted (AUG-2001) to the E
EMBL, AF406780, AAN03620.1; -
HSSP, P18614; LMHP.
                                                                                                                                                                   PRINTS; PR00453; VWFADOMAIN.
ProDom; PD000007; Clg_helix;
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339
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     65;
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                           Similarity
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                                                                                                                                             PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGRREDGG----PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGKSAKTAG--YEMHFGENGF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEPSTICAGESFQVVVRGNGF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNKGIATFAVGVGEYDISELKLIASGTDSTDRVFTVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDLGAIVYCVGVKDFNETQLARIA---DSKDHVFPVNDGFQALQGIIHSILKKSCIEILA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRI----QLQGYTTYTGRALQKVIRDFDDAYIGNKQVLLLLTDGQAKDNKLILP--NANRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQIYYENRQGYRT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AKLDIGKEIVRVGVVQYSHYVEGKSINKQKYITTEISIGEFKLLDNFENAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFSTRGTTLMKLTEDREQIRQGLEELQKVLPG------GDTYMHEGFERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNWRKEGSRNTECPS--SGVDVLFVLDGSGSVGKNFDKVKDWVKNIT-------
                                                                                               1626 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 1332 into
1332 AA; 145851 MW;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Integrin; Signal; Transmembrane
9.7%; Score 148.5; DB 2; 25.4%; Pred. No. 0.011; tive 45; Mismatches 105;
                                                                                               161115 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Burgeson R.E.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                        7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 153.5; DB Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       integrin alpha Hrl.
WW; 0D9108D2B05CFFAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                               34C68E3CFD467407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1626
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     Indels
                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1332;
                                                                                               CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                               1626;
  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT
Q8T5C3
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Q8T6U5
ID Q8T6U
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                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8T6U5 PRELIMINARY; PRT; 441 AA.

Q8T6U5;

Q1-JUN-2002 (TrEMBLrel. 21, Created)

Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)

Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Proximal thread matrix protein 1 variant a.

Mytilus edulis (Blue mussel).

Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;

Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;
                                                                                                                                                                                                                                                                                                                                                          Matrix protein. SEQUENCE 441
                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomacromolecules 3:1240-1248(2002).
EMBL; AF414454; AAL83537.1; -.
GO; GO:0005198; F:structural molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002035; VWF_A. Pfam; PF00092; VWA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           byssal fibers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Collagen-binding matrix proteins
               12
                                                            407
                                                                                                                     352
                                                                                                                                                                              296
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                                                                                                                                                                             QFGLKDYSSKAEIKGAID---KVTPSIIGQTAIGDGLENARLEV-FPNRNGGGREEVQKV
                                                          TSSFNKLSKIMENVVKLACM
                                                                                                                                                                                                                                    CAGHADIAFVEDASSSINANNPNNYGLMKDFMKDIVDRENKTGPDGTQFAVVTFADRATK
                                                                                      NDGFQALQGIIHSILKKSCI 194
                                                                                                                  VILLTDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-T 406
                                                                                                                                              IIALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPV 174
                                                                                                                                                                                                       LMKLTE--DREQIRQGLEELQKYLPG--GDTYMHEGFERASEQIYYENRQG---YRTASV 117
                                                                                                                                                                                                                                                                CYGGFDLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYSDRPTTAFELGLFGSQEEVKAAARRL--AYHGGNTNTGDALRYITARSFSPHAGGRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFSTRGTTLMK--LTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEITGFDLMDLFSVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRAYK--QVAILLTDGR-SQDLVLDAAAAAHRA---GIRIFAVGVGEALKEELEEIASEP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGCQAQRAGCKSVHYDLVFLLDTSSSVGKEDFEKVRQWVANLVDTFEVGPDRTRVGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVLCSFKINDSVTLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSAHVFHVSD-FNAIDKIRGKLRRRLCENVLC--PS-----VRVEGDRFKHTNGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPACYG-----GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFI
                                                                                                                                                                                                                                                                                                                                                        441 AA; 47543 MW;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                             9.7%;
                                                                                                                                                                                                                                                                                               46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
                                                                                                                                                                                                                                                                                                             Score 148; DB 2;
Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule activity; IEA
                                                          426
                                                                                                                                                                                                                                                                                                                                                          881D8BD36B891D2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elastomeric extraorganismic
                                                                                                                                                                                                                                                                                               77;
                                                                                                                                                                                                                                                                                                                             Length 441;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                  64
                                                                                                                                                                             351
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PROSITE;
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01-OCT-1996 (Rel.
25-OCT-2004 (Rel.
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    SEQUENCE
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                  Integrin alpha-M precursor (Cell su subunit) (CR-3 alpha chain) (CD11b)
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P11215;
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PS50234; VWFA; 2.
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Catarrhini;
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Pierce M.W., To
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Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 [1998].

-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iCD5 fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides of fibrinogen gamma chain.

-ISUSUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxvig C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assessment.";
Structure 6:923-935(1998)
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DOMAIN: The integrin I-domain (insert)
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                                                                             JO3925 AAA59411
JO3925 AAA599311
JO4145 AAA599311
JS52152 AAB248211
JS52153 AAB248211
JS52154 AAB248211
JS52155 AAB248211
JS52156 AAB248211
JS52161 AAB248211
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byssal fibers.";
Biomacromolecules 3:1240-1248(2002)
EMBL; AY053391; AAL17974.1; -.
                                                                                                              01-JUN 2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorph
                                 MEDLINE=22313036; PubMed=12425661;
Sun C., Lucas J.M., Waite J.H.;
"Collagen-binding matrix proteins i
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SMART; SM00327; VWA; 1.
                                                                   SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=29158;
                                                                                                                                                                                   Q8T5C2;
                                                                                                                                                                                             Q8T5C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
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PROSITE; PS50234; VWFA;
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Pfam; PF000357; Integrin_alpha;
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0008305; C:integrin complex; GO; GO:0007155; P:cell adhesion; TAS InterPro; IPR0000413; Integrin_alpha. InterPro; IPR002035; VWF_A.
                                                                                                      Mytiloidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01185; INTEGRINA. PRINTS; PR00453; VWFADOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                        DIAFLIDGSGSIIPHDFRRMKEFVST----VMEQLKKSKTLFS----LMQYSEEFRIH
                                                                                                                                                                                                                                                 VNN-FEALKTIQNQLREK----IFAIEGTQTGSSSSFEHEMSQEGFSAA
                                                                                                                                                                                                                                                                          VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA
                                                                                                                                                                                                                                                                                                  DGEKFGDPLGYEDVIPEADRE--
                                                                                                                                                                                                                                                                                                                       DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 173
                                                                                                                                                                                                                                                                                                                                             FTFKEFQNNPNPRSLVKPITQLL-
                                                                                                                                                                                                                                                                                                                                                                  -----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 122
                                                                                                                                                                                                                                                                                                                                                                                                              DLYFILDKSGSVL-HHWNBIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
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X-ray;
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X-ray;
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                                                                                                    Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                               PRELIMINARY;
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1152
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@=143-334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 145.5; DB Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Integrin alpha-M.
                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                  -GVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFQ
                                                                                                                                                                                                                                                                                                                                             - GRTHTATGIRKVVRELFNITNGARKNÅFKILVVIT
                                    from
                                                         DOI=10.1021/bm0255903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAS.
                                                                                                                                                                                               453
                                    elastomeric extraorganismic
                                                                                                                Pteriomorphia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                 Mytiloida;
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Best L
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                                                                                                                               ERRATUM.
CORbi A.L., Garc
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN STANDARD; PRT; 1163 AA.
P20702; QBIVA6;
01-FEB-1991 (Rel. 17, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion alpha chain) (Leukocyte adhesion receptor p150, alpha chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matrix protein.
SEQUENCE 453
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                                                                                                                                                                                                                                                                              Corbi A.L., Miller L.J., Commerce..., recture "cDNA cloning and complete primary structure leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002035; V
Pfam; PF00092; VWA; 2.
MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                            SEQUENCE
                                                                                                                                                                                                                      MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Sp
"Genomic structure of an integrin
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=88166645; PubMed=3327687;
Corbi A.L., Miller L.J., O'Connor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=ITGAX; Synonyms=CD11C;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VILLTDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-T 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMKLTE--DREQIRQGLEELQKVLPG--GDTYMHEGFERASEQIYYENRQG----YRTASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDGFQALQGIIHSILKKSCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGHADIAFVFDASSSINANNPNNYQLMKNFMKDIVDRFNKTGFDGTQFAVVTFADRATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPV 174
                                                                                                              FROM
                                                                                                                                                                                              Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 AA; 48784 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                       Garcia-Aguilar J., Springer
m. 265:12750-12751(1990).
                                                                                                                                                                                            265:2782-2788 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%;
25.5%;
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                                                                                                                                                                                                                       integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 145;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
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                                                                                                                                                                                                                                      Springer
                                                                                                                                                                                                                       alpha
                                                                                                                                                                                                                T.A.;
subunit, the leukocyte p150,95
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,95) (CD11c) (Leu M5)
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                                                                                                                                                                                                                                                                                                                    Springer T.A.;
e alpha subunit
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Lam; PF00435; Integrin_
Lam; PF01839; FG-GAP; 3

Pfam; PF00357; Integrin_alpha; 1.

DR Pfam; PF00952; VWA; 1.

DR PRINTS; PR01185; INTEGRIN*

PRINTS; PR01185; INTEGRIN*

R SMART; SW*

PPO**
                                                                                                                                             GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:000155; P:cell adhesion; TAS.
DR GO; GO:0009187; P:cell adhesion; TAS.
DR GO; GO:0009887; P:organogenesis; TAS.
DR InterPro; IPR000413; Integrin_alpha.
NR InterPro; IPR002015; VWF A.
R Pfam; PF01839; FG-GAP.
Pfam; PF01839; FG-GAP.
     Bosak S.A., McEwan P.J., McKernan K.J., Maramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences and p150,95 leukocyte adhesion proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 20-43.
MEDLINE=87167596; PubMed=3549901;
                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1N3Y; X-ray;
Genew; HGNC:6152;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A36584;
PDB; 1N3Y; X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain famil
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW, NOTE=CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. recognizes the sequence G-P-R in fibrinogen. It mediates cell-culture for the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the 
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L; M29165; -; NOT ANNOTATED CDS.
L; M29487; AAA51670.1; ALT SEQ.
L; M29482; AAA51620.1; JOINED.
L; M29483; AAA51620.1; JOINED.
L; M29484; AAA51620.1; JOINED.
L; M29485; AAA51620.1; JOINED.
L; M29486; AAA51620.1; JOINED.
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DOMAIN: The i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Predominantly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The integrin I-domain (insert) is a VWFA domain.
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     INTEGRIN ALPHA;
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Matches 55
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                                                                                                                                                             ch 9.4%;
l Similarity 24.8%;
55; Conservative '
                                                                              SLDYKD-VIPMADAAGIIRYAIGVGLAFONRNSWKELND----IASKPSQEHIPKVED-
                                                  LFFYSEREANRSRDLGAIVYCVGV-------KDFNETQLARIAD--SKDHVFFVNDG
                                                                                                                                     DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE--
FDALKDIONQLKEK----IFAIEGTETTSSSSFELEMAQEGF
                  FQALQGIIHSILKKSCIBILAAEPSTICAGESFQVVVRGNGF
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335
1163
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335
127886 MW;
                                                                                                                                                             ; Score 143.5; DB 1;
; Pred. No. 0.018;
43; Mismatches 89;
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                                                                                                                                                               89; Indels
                                                                                                                                                                                  Length 1163;
356
                   219
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                                                            177
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                                                                 DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein search, using sw model
                                                                                A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
     82654
                                                                                                                                                                                                                                                                                                                    2105692 seqs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                   GGFDLYFILDKSGSVLHHWN.....LQGIIHSILKKSCIEILAAE 187
geneseqp1980s:*
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Example 4; SEQ ID NO 2121; 10078pp; English. Novel nucleic acids and polypeptides, useful as central nervous system injuries.

for treating

disorders

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WPI; 2001-442253/47. N-PSDB; AAI58132.

Tang YT, Liu C, Asundi V, (Wang J, Wang Z, Wehrman T, Zhou P, Goodrich R, Drmanac

Chen R, Xu C, IC RT;

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Ren F, Zhang

Wang D; J, Zhao QA;

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961	961	961	961	965	965	965	970	970	970	970	970	970	970	970	970	970	970	970	970
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Abu54438	Abu54492	Abb90785	Abb90731	Ad177138	Abg63873	Aae01469	Adr48216	Adm64578	Adj70017	Adi00552	Abu54431	Abu54457	Abp54904	Abb90724	Abb90750	Adm64576	Adi00550	Adm64592	Adm64590
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21-JAN-2000; 2000US-00488725.
25-APR-20000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00652191.
14-SEP-2000; 2000US-00662191.
19-CCT-2000; 2000US-00663191.
19-CCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM38976;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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Best Local S
Matches 187
                                                                                                                                                                                (ROTT/)
(OKEE/)
(OZKA/)
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plasmid p0615; mutein.
                                                                         Rottman
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                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2002; 2002US-00201292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion; von Willebrand factor A-like domain; vWF; antibacterial; cutaneous; inhalation anthrax; human; TANGO 197 HisTag fusion; m
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                                                                                                                                           ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
                                                                         JB,
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Pred. No. 1.6e-99;
; Mismatches 0;
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                                                                             Healey JJ;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                     (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or amellorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor Adomain (vWF) amino acid sequence and an amino acid sequence heterology
                                                                                                                                                                                                                                                       antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein.
                                                                                                                                                                                                                                                                                                                         Human TANGO197-His tag fusion
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                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004
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                                                                                                                                                                                       US2003134786-A1
             Rottman
                                                                                                        20-DEC-2001; 2001US-00038307
                                                                                                                                 20-DEC-2001; 2001US-00038307
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                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein; 328
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             Ozkaynak E,
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Pred. No. 1.8e-99;
; Mismatches 0;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TANGO, 128, 140, 197, 212, 213, 224; 239, modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colities; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
                                                                                                                                                                                                                                                                                                                                      Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; sutoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
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   30-DEC-1998;
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                                                                 23-DEC-1999;
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Pred. No. 1.8e-99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus crythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, remumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid sequences encoding TANGO-128, and 239 polypeptides useful for the treatment of arthritis, psoriasis and autoimmune diseases.
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N-PSDB; AAA47455.
                                                                                                                                                                              Human anthrax toxin receptor.
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                                                                                                                                                                                                                                                ABP54905;
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                                                                Peptide
                                                                                                                                                Anthrax; toxin;
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                                 /label= Signal_peptide
28. .333
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Pred. No. 1.9e-99;
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asthma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as a human anthrax toxin receptor (ATR) polypeptide of the basis of cidentity to a newly isolated human ATR (see ABP54903). The 2 polypeptides are identical between amino acids 1-317, but differ thereafter at the C-care identical between amino acids 1-317, but differ thereafter at the C-care identical between amino acids 1-317, but differ thereafter at the C-care identical between amino acids 1-317, but differ thereafter at the C-care identical provides and provides and provides and provides and provides and provides and provides and polypeptides and college identification that it can be a complete or partial ATR. The invention provides ATR polypeptides and CC polynucleotides, vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the CC animals. It also provides methods for identifying molecules that bind the CC arithmethod for treating anthrax in a human or animal involves administering an agent CC treating anthrax in a human or animal involves administering an agent that inhibits binding between anthrax toxin protective antigen (PA) and ATR at a level effective to reduce the severity of anthrax. Suitable agents include the present polypeptide or a PA-binding fragment of it, a pa-binding polypeptide at least 80% identical to these, a fusion protein, a monoclonal or polyclonal antibody, a polysaccharide, a lipid or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young
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      fusion;
                                                               Human TANGO 197 protein.
                                                                                                                                  22-APR-2004
                                                                                                                                                                                                  ADI00534;
                                                                                                                                                                                                                                                           ADI00534 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 333 AA;
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      Willebrand
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      factor A-like domain;
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      VWF;
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      antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                           Human von Willebrand factor
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100.0%; Pred. No. 1.9e-99;
tive 0; Mismatches 0;
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                                                           A-like domain protein TANGO197
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heterologous
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antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vWF amino acid sequence; anthrax; Bacillus anthracis; cu

cutaneous

anthrax;

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RESULT 8
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Best Local Sim.
Matches 187;
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described ser: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a human von Willebrand factor A-like domain (vWF) amino acid sequence TANGO197.
                               Human TANGO 197
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                                                                                                                                       ADI00554;
                                                                                   22-APR-2004
                                                                                                                                                                                        ADI00554 standard; protein;
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DB; ADM64567.
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Pred. No. 1.9e-99;
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor Adomain (vWF) amino acid sequence and an amino acid sequence heterolog to the vWF.
                                         03-JUN-2004
                                                                                            ADM64580
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                                       (first entry)
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Pred. No. 1.9e-99;
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Human TANGO197-FLAG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax; inhalation anthrax; human; TANGO197; FLAG; fusion protein; gene.
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               ADI00556;
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(OKEE/)
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liorating symptoms of anthrax comprises a von Willebrand factor A-lik
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HEALEY J J.
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Pred. No. 1.9e-99;
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                                                                                                                                                                                                                                              The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 HiaTag fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                        New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                          Claim 45; SEQ ID NO 24; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2002; 2002US-00201292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003144193-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cutaneous;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion; von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROTT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OZKA/)
                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-720708/68.
                     181
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221
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O'KEEFE T L.
OZKAYNAK B.
HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        JB,
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       ADI00555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p0614;
                                                                                                      QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                               GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
                                                              SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                       QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                  GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLKMSFIVFSTRGTTLMKLTEDRE
                                                                                                                                                                                                                            345 AA;
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IEILAAE
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  inhalation anthrax; human;
614; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 HisTag fusion
                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombin cleavage site
                      187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Wild-type"
                                                                                                                                                                                           100.0%;
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Pred. No. 2e-99;
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; TANGO 197 HisTag
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                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                  0
                                                                                                                                                                                                      Length 345;
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                                                                                                                                                                                                                                                                       The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising human TANGO197, thrombin cleavage site and his tag that can be used to treat exposure to or prevent a symptom of anthrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ameliorating symptoms of anthrax domain (vWF) amino acid sequence
                                                                                                                                                                                                                                                 Sequence 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 44; SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWP amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein; gene.
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DB; ADM64581.
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                                                                                                                                                                        Similarity
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                                          SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSC 180
                                                                              QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                       QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                       SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                                                                     GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
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                                                                                                                                                                                          Score 970; DB 7
Pred. No. 2e-99;
; Mismatches
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ARESULT 12
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AC ABP54
AX ABP54
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CFT Pepti
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FT Domai
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                                                  Novel isolated polypeptide useful for identifying reduces effect of anthrax toxin on host cell, for
                                                                                                                                                                                                                                                                                                                                             Region
                     Claim 1;
                                                                                   N-PSDB; ABV73881.
                                                                                                                                                            05-DEC-2000; 2000US-0251481P
                                       human animal suffering from anthrax.
                                                                                             WPI; 2002-713235/77.
                                                                                                                                                                                03-OCT-2001; 2001WO-US030941
                                                                                                                                                                                                      13-JUN-2002.
                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human anthrax toxin receptor
                                                                                                                                       (WISC ) WISCONSIN ALUMNI
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                                                                                                                  JAT,
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                    Page 29-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                 Bradley KA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; human; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "PA-binding fragment, begins at any amino acid in
the range 27-43 and ends at any amino acid in the range
221-321, region specifically described in Claim 3"
                                                                                                                                                                                                                                                                                         /note= "forms metal ion-dependent a
motif with amino acid residues 50,
                                                                                                                                                                                                                                                                                                                         /note= "forms metal ion-dependent
motif with amino acid residues 50,
                                                                                                                                                                                                                                                                                                                                                        /note= "forms metal ion-dependent
motif with amino acid residues 50,
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notif with amino acid residues 50, 54, 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "forms metal ion-dependent adhesion
notif with amino acid residues 52, 54, 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label Signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Mature_protein
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                   45pp;
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                                                                                                                                                                                                                                                                     "putative transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "von Willebrand
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                                                                                                                                                                                                                                                "cytoplasmic
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), 52, 54 a
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and 150"
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present sequence is the protein sequence of a

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Best Local S
Matches 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anthrax toxin receptor (ATR), as predicted from an isolated cDNA clone. Anthrax toxin protective antigen (PA) binds to the ATR at a von Willebrand factor A domain located in the extracellular domain of ATR. The invention provides ATR polypeptides and polymucleotides, vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent that inhibits binding between PA and ATR at a level effective to reduce the severity of anthrax. Sultable agents include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at least 80% identical to these, a fusion protein, a monoclonal or polyclonal antibody, a polysaccharide, a lipid or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; immunoglobulin G; IgG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 368 AA;
     N-PSDB;
                                                                                       Rottman
                                                                                                                                                                      (ROTT/)
(OKEE/)
(OZKA/)
                                                                                                                                                                                                                                                                                      20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                                                             20-DEC-2001; 2001US-00038307.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                         ROTIMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                                                       Ozkaynak E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising human TANGO197 extracellular region, minus the DG residues closest to the transmembrane region, and immunoglobuling (IGG) fragment of crystallisation (FC) with mutations
                                                                                                                                                 foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; coll culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 384 AA;
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                                                                                                                                                                                                                                                                                                                                             Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
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                                                                                                                                    chromosome 19
                 Protein
                                                 Peptide
                                                                                                     Homo sapiens.
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                                                                   Location/Qualifiers
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Pred. No. 2.3e-99;
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CC Pathological conditions can be diagnosed by determining the amount of the constitutions can be diagnosed by determining the amount of the constitutions can be diagnosed by determining the amount of the constitutions in the new genes. Specific uses are described for each of the 28 genes, considered to the tissues in which they are most highly expressed, and include the new genes. Specific uses are described for each of the 28 genes, considered the constitution of proliferative constitutions, foetal and developmental abnormalities, autoimmune considered disorders, diseases of the immune system, AIDS, autoimmune constitution of the                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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30-JUN-2000; 2000US-0215133P.
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                                                                                                                                    SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 180
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               IEILAAE 187
                                                                                     SEREANRSRDLGAI VYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 970; DB 4;
Pred. No. 2.4e-99;
; Mismatches 0;
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tein fragments or variants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                    Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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25-APR-2000;
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			Sequence 3,	Sequence 3,	Patent No. 5424399			Seguence 43,	Sequence 5, Appl:	Sequence 53,	Sequence 53,	Sequence 53,	Sequence 53,	Sequence 53,	Sequence 53,	Sequence 53,	octuerice 22,

# ALIGNMENTS

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; SEQUENCE CHARACTERISTICS;
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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GENERAL INFORMATION:
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TELEX: 224401
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Gateway 2000 P5-90

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04439
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Darnley, James D., Jr.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4767
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/385-5210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAC-1 I-DOMAIN PROTEIN USEFUL IN TITLE OF INVENTION: BLOCKING ADHESION AND MIGRATION OF NEUTROPHILS NUMBER OF SEQUENCES: 9
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Heinrikson, Robert L.
Anderson, Donald C.
Tomich, Che-Shen C.
Tomich, Che-Shen C.
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                                                                                                                                                        Query Match
Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION UNMBER: 938,659
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STREET: Chicago
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                                                                                                                                                                                                                                                                                                                     TELEPAX: 25-3856
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/173,497
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                                                                                                   4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
                               DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIHFTFKEFONNPNPRSLVKPITOLL--GRTHTATGIRKVVRELFNITNGARKNAFKILV
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                                                                                                                                      14.6%;
ilarity 27.7%;
Conservative 3
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                                                                                                                                          38;
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                                                                                                                                      Score 141.5; DB 1;
Pred. No. 4.5e-07;
38; Mismatches 75;
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e, 6300 Sear Tower
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                                                                                                                                                                         Length 1151;
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                                                                                                                                        Gaps
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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                  Matches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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ADDRESSEB: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
LENGTH: 1151 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 167
                                                                                                                                           142
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                                                            DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
                                                                                                 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
                                                                                                                                         DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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7: United States
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                                                                                                                                                                                                                                    14.6%;
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                                                                                                                                                                                                                    Score 141.5; DB 1
Pred. No. 4.5e-07;
8; Mismatches 75
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                                                                                                                                                                                                                                                           Length 1151;
                                                                                                                                                                                                                      Indels
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; MOLECULE TYPE: protein
US-08-362-652-37
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                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino aci
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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 313
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                                                                                                   LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 167
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                                   LOGIIHSILKK 178
                                                                  PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
LRSIQRQLQEK 323
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Pred. No. 4.5e-07;
8; Mismatches 75; Indels 25;
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US-08-605-672-37
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                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Gallat
APPLICANT: Van de
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-1.
TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                    168
                                                                                                              117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFVNDGFQA 167
                                                                                                                                                    202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                                                                                                                              142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
                                                                                                                                                                                        58 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
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                                    LOGIIHSILKK 178
                                                                            PLBYSDVIPAADKA---
LRSIQRQLQEK 323
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       protein
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27.7%; Pred. No. 4.5e-07;
tive 38; Mismatches 75
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RESULT 6
US-08-482-293A-37
RESULT 7
US-08-943-363-37
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Best Local :
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APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: STREET: Chicago
CITY: Chicago
TMATE: Illinois
TMATE: Thited
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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PRIOR APPLICATION UMBER: US 08/173,497
PILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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                                                                                                           LQGIIHSILKK 178
                                                                       LRSIQRQLQEK 323
                                                                                                                                                                                                                       DPQSLVDPIVQLQ---
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233 South Wacker Drive, 6300 Sear Tower
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27.7%; Pred. No. 4.5e-07;
1tive 38; Mismatches 75;
                                                                                                                                               -GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                                                                                                                                       GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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Best Local Similarity
Matches 53; Conserv
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APPLICANT: Gallatin,
APPLICANT: Van der Vi
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PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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NAME: Williams Jr., Joseph J
REGISTRATION NUMBER: 38,659
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                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 312-474-0448
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OPERATING SYSTEM: PC-DOS/MS-DOS
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313
                                                                                                    117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFVNDGFQA 167
                                168 LOGIIHSILKK 178
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LRSIQRQLQEK 323
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233 South Wacker
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                                                                                                                                                                                                                                                                                14.6%; Score 141.5; DB 2
27.7%; Pred. No. 4.5e-07;
7ative 38; Mismatches 75
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5837478el Human
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RESULT 8 US-09-193-043-37

Sequence 37, Application US/09193043 Patent No. 6251395

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GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: NO. 62513961 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
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ORGANISM: Rattue rattue

US-09-193-043-37
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PRIOR FILING DATE: 1998-11-16
PRIOR PELICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Mon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/09688307A
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                                                                      SOFTWARE: PA
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TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
                                                                                                                      PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
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SOFTWARE: Patentin Ver.
                          LENGTH: 11
TYPE: PRT
ORGANISM: Rattus rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168
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                                                                                                   Patentin Ver.
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; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-350-259-37
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                                                                                                    CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/13,043
EARLIER FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/363,363
EARLIER FILING DATE: 1994-10-03
EARLIER FILING DATE: 1997-10-03
NUMBER: 0F SEQ ID NOS: 114
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                                                                       SOFTWARE: PatentIn SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37, Appl
Patent No. 662091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915el Human 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa = NAME/KEY: misc feature LOCATION: 1117
OTHER INFORMATION: Xaa = NAME/KEY: misc feature LOCATION: 1118
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 27866/35004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KBY: misc_feature
LOCATION: 464
OTHER INFORMATION: Xaa =
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRSIQROLQEK 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DREQIRQGLBELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
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Pred. No. 4.5e-07;
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201 57

Best Local Similarity

14.6%;

Pred. No. 4.5e-07;

Length 1151;

Query Match

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167

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RESULT 11
US-08-485-618-55
                                                                                               US-08-485-618-55
                                                                                                                                             TELEPAX: 312--..
TELEPAX: 25-3856
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
"FNGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 55, Application US/08485618 Patent No. 5728533
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                     Matches
                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MERAL INFORMATION W. MICHAEL APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5728533el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
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CITY: Chicago
Illinois
Inted
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                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                      Local Similarity
                                                                                                                                                                                                                                                                                                   NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                TELEPHONE:
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233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
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                   Conservative
                                                                                                              protein
               14.6%; Score 141.5; DB 1
27.7%; Pred. No. 4.5e-07;
tive 38; Mismatches 75
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e, 6300 Sear Tower
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                                                      DB 1;
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US-08-362-652-55
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                                                                                                                                Query Match
Best Local Similarity
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Patent No. 5
                                                                                                                  Matches
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                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 5-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
                                                                                                                                                                                                                                     LENGTH: 1161 amır
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312-474-0448
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STATE: Illino:
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
                                        152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
   58 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
                                                                                                                53;
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                                                                           4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                                                                                                                                  1161 amino acids
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                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vieren, Monica
No. 5766850el Human 2 Integrin Alpha Subunit
                                                                                                            14.6%; Score 141.5; DB 1;
27.7%; Pred. No. 4.5e-07;
27.7%; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W. Michael
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cker Drive, 6300 Sear Tower
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                                                                                                                                                 Length 1161;
                                                                                                                  Indels
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/ MOLECULE TYPE: protein

US-08-605-672-55
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US-08-605-672-55
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acid
                                                                                                                                                         Query Match 14.6%; Score 141.5; DB 2; Length 1161; Best Local Similarity 27.7%; Pred. No. 4.5e-07; Matches 53; Conservative 38; Mismatches 75; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/08605672 Patent No. 5817515
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                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
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CORRESPONDENCE ADDRESS:

CORRESPONDENCE Marshall, O'Toole, Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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PRIOR APPLICATION UNDARA:
APPLICATION UNDARR: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                 4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                    DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
                                                                            DIAFLIDGSGSINGRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
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DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
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e, 6300 Sear Tower
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                                                                                                                                                           Gaps
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US-08-482-293A-55
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GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 23-DEC-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-DEC-1994
ATTONNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human
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                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312-4.
                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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CITY: Chicago
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117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFVNDGFQA 167
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                                                                                                                  152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
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                                                                         58 DREQIRQGLEBLOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
                                                                                                                                                     4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                                                                                                             Similarity
53; Conserv
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                                    DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                            14.6%; Score 141.5; DB 2
27.7%; Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/482,293A
                                                                                                                                                                                           38;
                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                              Length 1161;
                                                                                                                                                                                             Indels
                                                                                                                                                                                             25;
                                                                                                                                                                                             Gaps
                                                                                                                  211
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-55
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US-08-943-363-55
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/362,652
PILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 312-474-630
TELEPAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                    Match 14.6%; Score 141.5; DB 2; Local Similarity 27.7%; Pred. No. 4.5e-07; les 53; Conservative 38; Mismatches 75;
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    267
                                              117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
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                                                                                        212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
                                                                                                                                                                                152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
                                                                                                                                  58 preqirqgleelokvlpggdtymhegferaseqiyyenrqgyrta-sviialtpgelheb 116
                                                                                                                                                                                                                          4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
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233 South Wacker Drive, 6300 Sear Tower
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                       and is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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US-10-038-307-26
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US-99-796-753-12
US-10-038-307-2
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US-10-038-307-24
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Sequence 54, Appl	equence 16	equence 6,	quence 6,	quence 52	99	16,	e 14,	w	16,	14,	•	12,	12,	e 30,	e 301,	e 194,	e 301,	e 194,	e 620,	e 232,	e 187,	equence 1823	e 199,	equence 20,	e 20,	equence 232,	equence 187,	e 18,	e 18,	Sequence 36, Appl	e 34,	,2

# ALIGNMENTS

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SOPTWARE: PRETSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-26
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US-10-038-307-26
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Publication No. US20030134786A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEPE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILLING DATE: 2002-06-28
                                                                                                                                                                                                                           V Match 100.0%; Score 970; DB 14; Local Similarity 100.0%; Pred. No. 6e-93; nes 187; Conservative 0; Mismatches 0;
                                             101
121 SERBANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 180
                                                                                        61 QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY 120
                                                                                                                                        41
                                                                                                                                                           1 GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE 60
                                                                                                                                   GEPDLYPILDKSGSVLHHWNBIYYFVBQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE 100
                                           QIRQGLEBLQKVLPGGDTYMHEGPERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY 160
                                                                                                                                                                                                                                                                           DB 14; Length 328;
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APPLICANT: Judith J. HEALEY
ITITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILIN DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-26
         APPLICATION NUMBER: U9/23,546
PRIOR APPLICATION NUMBER: U9/23,546
PRIOR APPLICATION NUMBER: U9/23,994
PRIOR APPLICATION NUMBER: 09/23,994
PRIOR APPLICATION NUMBER: 09/23,994
PRIOR APPLICATION NUMBER: 09/23,994
PRIOR PILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/23,546
PRIOR APPLICATION NUMBER: 09/23,546
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PRIOR APPLICATION NUMBER: 09/23,546
PRIOR APPLICATION NUMBER: 09/23,546
PRIOR APPLICATION NUMBER: 09/23,546
PRIOR APPLICATION NUMBER: 09/23,546
PRIOR APPLICATION NUMBER: 09/24,246
PRIOR PILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR APPLICATION NUMBER: 60/123,458
PRIOR APPLICATION NUMBER: 60/123,458
PRIOR APPLICATION NUMBER: 60/123,458
PRIOR APPLICATION NUMBER: 60/123,458
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US-09-796-753-12
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US-10-201-292-26
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                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09796753 Publication No. US20030027998A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
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PRIOR APPLICATION NUMBER: (PRIOR FILING DATE: 2000-09-
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 12
LENGTH: 333
                                                                   RESULT 4
US-10-038-307-2
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; ORGANISM: Homo sapiens
US-09-796-753-12
Sequence 2, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 187; Conservative
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FILING DATE: 1999-12-29
APPLICATION NUMBER: 09/514,010
FILING DATE: 2000-02-25
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FILING DATE: 1999-12-23
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APPLICATION NUMBER:
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60

160

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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEPE

APPLICANT: Engin OXAYYAK

APPLICANT: Judith J. HEALEY

ITITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REPERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 333

TYPE: PRT

ORGANISM: Homo sapiens
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US-10-201-292-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-2
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Best Local Similarity
Matches 187, Conserv
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SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 187; Conservative
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APPLICANT:
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CURRENT FILING DATE: 2002-06-28
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  161
                      121 SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSC 180
                                                                          101 QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
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                                                                                                61 QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
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SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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Judith J. HEALEY
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                                                                                                                                                                                                                                               100.0%; Score 970; DB 14; Length 333; 100.0%; Pred. No. 6.2e-93;
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNA;
APPLICANT: Engin OZKAYNA;
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE: PAT
ORGANISM: Homo sapiens
US-10-038-307-22
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US-10-201-292-22
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                                                                          ORGANISM: Homo sapiens US-10-201-292-22
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                                                                                                                        Query Match 100.0%; Score 970; DB 14; Best Local Similarity 100.0%; Pred. No. 6.4e-93; Matches 187; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 970; DB 14; Best Local Similarity 100.0%; Pred. No. 6.4e-93; Matches 187; Conservative 0; Mismatches 0;
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                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                      Application US/10201292
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                                      DB 14;
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220 180 160 120 100 60 0

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Sequence 24, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTWAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14
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US-10-038-307-24
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US-10-038-307-24
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LENGTH: 345
TYPE: PRT
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Publication No. US20030134786A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-12
; PRIOR RELING DATE: 2000-02-6, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOPTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 621
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621
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Publication No. US20
GENERAL INFORMATION:
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Best Local 8
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LENGTH: 345
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TITLE OF INVENTION: Albumin Fusion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PF546PCT
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                             IBILAAE 227
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o. US20040010134A1
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; ORGANISM: Homo sapiens
US-10-201-292-32
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                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
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                                                                                                                                                         Query Match 100.0%; Score 970; DB 1
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 187; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Bigin OZKAYNAK
APPLICANT: Bigin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKANAK
APPLICANT: Udith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-953-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
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ORGANISM: Homo sapiens
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APPLICANT: James B. ROTTMAN
APPLICANT: Therees L. O'KEEFE
APPLICANT: Therees L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 504
TYPE: PAT
ORGANISM: Homo sapiens
US-10-201-292-34
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Wir
; SEQ ID NO 36
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-201-292-36
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US-10-201-292-36
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US-10-201-292-34
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Publication No. US20030144193A1
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                                                                                                                                   APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NOMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
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                                                                                                           Windows Version 4.0
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Pred. No. 1.1e-92;
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Sequence 18, Application US/10038307

Publication No. US20030134786A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theress L. O'KEEFE

APPLICANT: Engin OZKAYNA;

APPLICANT: Theress L. O'KEEFE

APPLICANT: UJUITEN J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-2959

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

$EQ ID NO 18

LENGTH: 551

TYPE: PRT

ORGANISM: Homo Bapiens
Search completed: June 13, 2005, 20:36:50 Job time: 59.9593 secs
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US-10-038-307-18
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seq length: 2000000000
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	<sub>U</sub>	4	w	N	_	NO.	Result
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collagen alpha 3(V	integrin alpha-E c	ondin-re	cartilage matrix p	e surfac	cartilage matrix p	cartilage matrix p	o.	collagen alpha 2(V	collagen alpha 2(V		hypothetical prote	m	ical pro	alpha	collagen alpha 1(V	type XII collagen	nt facto	alpha 1	alpha	alpi	hypothetical prote		leukocyte surface			2	cell surface glyco	antigen Eml00 - Ei	Description	

RWHUIB

cell surface glycoprotein CD11b precursor [validated] - human
cell surface glycoprotein CD11b precursor [validated] - human
N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004

protein

Mac

						RESULT 1
	ALIGNMENTS					
DNA gyrase, subun:	D85862	۵	875	8.7	84.5	<b>4</b> 5
DNA gyrase subunit	B91018	N	875	8.7	84.5	44
DNA topoisomerase	ITECAP	۳	875	8.7	84.5	43
endoglucanase homo	AB1079	2	800	8.7	84.5	42
probable retroelem	F84811	N	689	8.7	84.5	41
hypothetical prote	T05901	N	1021	8.8	85	40
hypothetical prote	H90261	N	380	8.8	85.5	39
hypothetical prote	B83262	N	340	8.8	85.5	38
hypothetical prote	AG2285	N	710	9.0	87	37
hypothetical prote	AG2350	N	418	9.0	87.5	36
hypothetical prote	T32949	N	341	9.0	87.5	35
valine-tRNA ligase	T30889	N	1218	9.1	88	34
inter-alpha-inhibi	JC5953	ผ	932	9.1	88.5	33
collagen alpha 3(v	A37797	N	3137	9.5	92.5	32
hypothetical prote	E70121	N	340	9.6	93	31
undulin 1 - human	A40970	N	843	9.6	93.5	30

### A;Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891 A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777) F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2> F;238-296/Domain: thrombospondin type 1 repeat homology <THR1> F;309-371/Domain: thrombospondin type 1 repeat homology <THR3> F;372-432/Domain: thrombospondin type 1 repeat homology <THR3> F;472-432/Domain: thrombospondin type 1 repeat homology <THR3> F;433-493/Domain: thrombospondin type 1 repeat homology <THR5> F;494-556/Domain: thrombospondin type 1 repeat homology <THR6> ई 밁 8 밁 S 밁 R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G. Mol. Biochem. Parasitol. 57, 171-174, 1993 A;Title: Sequence of a major Eimeria maxima antigen homologous A;Reference number: A48569; MUID:93149203; PMID:8426611 C;Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004 C;Accession: A48569 antigen Em100 - Bimeria maxima C;Species: Eimeria maxima δ A; Residues: 1-724 < PAS> A;Status: preliminary A; Molecule type: nucleic acid A;Accession: A48569 Query Match Best Local S Matches Local Similarity 218 165 107 117 LFFYSERB-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP--VNDG 164 61 47 53; 4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 60 WGGVSSQINGIIKAACKDL 236 QIRQGLEBLQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 116 FQALQGIHSILKKSCIEI 183 ----SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPRYLQSN 217 DVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDLSDSRA 106 QNADILAAAAKKI.PYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDGA----Conservative 14.1%; 26.6%; 38; Mismatches Score 137; DB 2; Lengu. .... Pred. No. 0.0007; ""smatches 80; Indels Length 724; ő 28; the Eimeria tenella mi Gaps

Residues: 1-9 <RES>

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A;Crobs-references; Us:MID(94
R;Hickstein, D.D.; Hickey, M.J; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence
A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218
A;Molecule type: mRNA
A;Residues: 9-1153 <HIC-
A;Cross-references: GB:J04145; NID:g189098893; PMID:2563162
A;Accession: A32218
A;Molecule type: mRNA
A;Residues: 9-1153 <HIC-
A;Cross-references: GB:J041415; NID:g1890889; PMID:2563162
A;Cross-references: GB:J041415; NID:g1890889; PMID:AAA59903.1; PMID:g386975
A;Note: part of this sequence was confirmed by protein sequencing
R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the nduring evolution.
A;Reference number: A46526; MUID:93123748; PMID:8419480
A;Accession: A46526
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A;Accession: A31108
A;Accession: A31108
A;Accession: A31108
A;Residues: 1-1153 <COR>
A;CORS—references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
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A;CORS—references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
R;Arnaout; M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor M
A;Reference number: A28915; MUID:88257215; PMID:2454931
A;Reference number: A28915; MUID:88257215; PMID:2454931
A;Accession: A28915; MUID:88257215; PMID:2454931
A;Coss-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A;Rote: the authors translated the codon TAC for residue 1129 as Thr
A;Note: part of this sequence, including the amino end of the mature protein, was confir
A;Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A;Accession: A41600; MUID:92073318; PMID:1683702
A;Accession: A41600; MUID:92073318; PMID:1683702
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A; Molecule
                                     A;Accession: I52567
A;Status: translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:M18044
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A; Residues: 917-1042 < AR2>
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A; Residues: 1-9 <SHE>
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                                          from
                                          GB/EMBL/DDBJ
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A;Residues: 1-9 <RES:
A;Cross-references: (
C;Comment: A common l
C;Genetics:
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; magr
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1183/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F;17-1109/Domain: extracellular #status predicted <EXT'>
F;17-1109/Domain: von Willebrand factor type A repeat homology <VWA2>
F;465-473/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-601/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted <INT>
F;86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: fibrochimerin
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A40020; A34485; B34405; A28037; S23814; S22254; S28811
C;Accession: A40020; A34485; B34405; A28037; S23814; S22254; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nish.
J. Cell Biol. 115, 209-221, 1991
                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-3124 <YAM>
A;Residues: 1-3124 <YAM>
A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g22281
A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A;Title: Type XII collagen. A large multidomain molecule with partial homology to type A;Reference number: A34485; MUID:90062079; PMID:2584192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete primary structure of type XII collagen shows a chimeric molecule wi nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site. A;Reference number: A40020; MUID:92011862; PMID:1918137
A;Accession: A40020
A;Accession: A40020
A;Accession: A40020
A;Accession: A40020
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by
                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID (211284; PIDN:AAA48635.1; PID:g211285
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A;Gene: GBB:ITGAM; CR3A
A;Cross-references: GDB:120599;
A;Map position: 16p11.2-16p11.2
                                                                                                        A; Molecule type: protein A; Residues: 2772-2792; 2846-2873
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                                                                                                                                                                           A;Accession: B34485
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F;12-3] Domain: signal sequence #status predicted <SIG>
F;24-3124/Product: collagen alpha 1(XII) chain #status predicted <FGSG>
F;24-3124/Product: collagen alpha 1(XII) chain #status predicted <MATS F;24-3124/Product: collagen alpha 1(XII) chain #status predicted <MATS F;24-114/Domain: IIIA #status predicted <IIIA>
F;24-114/Domain: fibronectin type III repeat homology <FN3A>
F;34-105/Domain: von Willebrand factor type A repeat homology <VWA1>
F;332-425/Domain: fibronectin type III repeat homology <FN3B>
F;332-414/Domain: fibronectin type III repeat homology <FN3B>
F;437-601/Domain: von Willebrand factor type A repeat homology <VWA2>
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F;630-711/Domain: fibronectin type III repeat homology <FN3B>
F;918-995/Domain: fibronectin type III repeat homology <FN3B>
F;912-895/Domain: fibronectin type III repeat homology <FN3B>
F;905-986/Domain: fibronectin type III repeat homology <FN3B>
F;905-1076/Domain: fibronectin type III repeat homology <FN3B>
F;108-1169/Domain: fibro
                                                                                                                                         F;2325-2490/Domain: von willeuram laccompleted
F;2438-2440/Region: cell adhesion #status predicted
F;2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status
F;2509-2750/Domain: collagenous COL2 #status predicted <COL2>
F;2912-2902/Domain: collagenous COL2 #status predicted <NC2>
F;2903-2945/Domain: non-collagenous NC2 #status predicted <COL1>
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F;3046-3048/Domain: collagenous COL1 #status predicted <NC1>
F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
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F;3049-3124/Domain: non-collagenous NC2 #status predicted <NC1>
F;3049-3124/Domain: no
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A; Residues: 2831-2832,'T', 2834,'R', 2836-2843;3002-3014 <
R; Trueb, J.; Trueb, B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A; Title: The two splice variants of collagen XII share a
A; Reference number: $28811; MUID:93042014; PMID:1420368
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A,Residues: 1-24,1189-1257,'8',1259-1263,'E',1265-1280 <TRU>
A,Cross-references: EMBL:X67327
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J. Blol. Chem. 262, 17724-17727, 1987
A;Tille: Type XII collagen is expressed in embryonic chick tendons.
A;Reference number: S22254; MUID:88087065; PMID:3121603
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A, Title: A major oligomeric fibroblast proteoglycan identified A, Reference number: S23814; MUID:92362621; PMID:1323460
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A;Note: this sequence has been revised in reference A34485
R;Koch M.; Bernasconi, C.; Chiquet, M.
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C;Reyworde: alternative splicing; cell binding; coiled coil; connective t
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A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 2960-2976, 'F', 2978-3074, 'AG' <GOR3>
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A;Accession: A28037
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     Local Similarity
     13.3%;
28.2%;
     Score 129;
Pred. No. (
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           0.02;
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992
C;Accession: A36584; A35543; S00864
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
RWHU1C
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F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR3>
F;372-432/Domain: thrombospondin type 1 repeat homology <THR4>
F;433-493/Domain: thrombospondin type 1 repeat homology <THR4>
F;494-556/Domain: thrombospondin type 1 repeat homology <THR5>
F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:043981; GB:AF032905; GB:M73495; NID:g2707732; PIDN:AAD03350 A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756) F;48-218/Domain: von Willebrand factor type A repeat homology <VWAI>
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A; Residues: 1-712 < TOM>
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C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994
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ol. Biochem. Parasitol. 49, 277-288, 1991
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
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216 SNWSNVTQQVNGIIKAACKDL 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 NRVKDIIQAINTFPYRGGSTNTGKAMTYVREKVFVTSK-GSRPNVPRVMILITDGK-SSD
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                                                                                         LVMTDGA--SNLPSQTRSSAAALRDAGATVVVLGVGSGVNSSECRSTAGCSTSNCPRYLQ
                                                                                                                                   IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP--VN 162
                                                                                                                                                                                KVRWNLSDPKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLV 157
                                                                                                                                                                                                                             QIRQGLEELQKVLPG----
                                               DGFQALQGIIHSILKKSCIBI 183
                                                                                                                                                                                                                                                                                                                       DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDRE
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Pred. No. 0.0037;
Pred. No. 0.0037;
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protein CD11c precursor - hum leukocyte adhesion receptor

human

p150,95 alpha chain

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leukocyte surface glycoprotein Mac-1 alpha chain precursor - N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence revision 30-Sep-1991 #text_charC;Accession: S00551; I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: this sequence has been revised in 1 R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; EMBO J. 6, 4023-4028, 1987
A;Title: cDNA cloning and complete primary A;Reference number: S00864; MUID:88166645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: this revision to the sequence from reference A35543 includes the R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A. J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit, the leukocyte pl A;Reference number: A35543; MUID:90153906; PMID:2303426
A;Accession: A35543
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A;Molecule type: DNA
A;Residues: 1-1163 <COR>
A;Cross-references: UNIPROT:P20702
                  A; Title: Amino acid sequence of the murine A; Reference number: S00551; MUID:88312584;
                                                          R;Pytela, R.
EMBO J. 7, 1
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A; Accession: S00551
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A; Residues: 1-755, 'L',
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A; Residues: 1-834 < CO2>
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                                                                                                                                                                                                                                                                                                                                                                                       117 LFFYSEREANRSRDLGAIVYCVGV-------KDFNETQLARIAD--SKDHVFPVNDG 164
                                                          1371-1378,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
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                                                                                                                                                                                                                                                                                                               FOALOGIIHSILKK 178
                                                                                                                                                                                                                                                                                                                                                   SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND----IASKPSQEHIFKVED-
                                                                                                                                                                                                                                                                                                                                                                                                                             NPLSLLASVHOLO-----GFTYTATAIONVVHRLFHASYGARRDATKILIVITDGKKEGD
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                                                                                                                                                                                                                                                                         FDALKDIQNQLKEK 332
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                                                            1988
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K.; Larson, R.S.; S
                    Mac-1 alpha chain
PMID:3044779
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                                                                                                              #text_change 09-Jul-2004
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                                      reveals homology with the
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A;Molecule type: mRNA
A;Residues: 660-677, 'R',679,681-723,'G',725
A;Cross-references: GB:M16271; NID:g199289;
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                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1; FR;Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R.
J. Biol. Chem. 265, 19040-19046, 1990
A;Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different mer A;Reference number: A36593; MUID:91035430; PMID:2229060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A38876; B36593; I54429
R;Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, submitted to GenBank, January 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A38876; B36593; I54429
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand C;Keywords: cell adhesion; glycoprotein; transmembrane protein
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                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                           A; Title: DNA polymorphism of MHC III genes A; Reference number: 154429; MUID:87192938;
                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-760 < ISH>
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A; Residues: 1-760 < IS2 >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) N;Alternate names: C3 convertase; C5 convertase; complement
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  <RES>
PIDN:AAA39562.1;
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     PID:g199290
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C;Genetics: 16/1
A;Introns: 16/1
C;Complex: The I
C;Function:
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A;Reference number: $42368
A;Accession: $42373
A;Molecule type: DNA
A;Residues: 1-3051 <SMI>
A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T20G5.3 - Caenorhabditis elegans C/Species: Caenorhabditis elegans C/Species: Caenorhabditis elegans C/Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004 C/Accession: S42373
R/Smith, A.
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F)19-250/Product: complement C2b fragment #status predicted <C2B>
F)22-89/Domain: complement factor H repeat homology <FH1>
F)24-149/Domain: complement factor H repeat homology <FH2>
F)156-210/Domain: complement factor H repeat homology <FH2>
F)251-760/Product: complement C2a fragment Borm #status predicted <C2A>
F)251-605,613-760/Product: complement C2a fragment short form #status predicted <C2A>
F)259-449/Domain: von Willebrand factor type A repeat homology <VFA>
F)259-449/Domain: von Willebrand factor type A repeat homology <VFA>
F)478-747/Domain: trypsin homology #status stypical <TRY>
F)478-747/Domain: trypsin homology #status atypical <TRY>
F)479-89,94-116,122-149,156-197,182-210,470-590,499-515,593-609,647-674,685-715/Dis
F)27,117,297,340,474,478,663/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                          A;Introne: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1 F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1> F;754-793/Domain: fibronectin type II repeat homology <2F1>
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A;Pathway: complement classical pathway
C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology;
C;Keywords: alternative splicing; complement classical pathway; duplication; glycoprote
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
                                                                                                                                                                                                                                                                                                                                                                             1201-1244/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               570,689/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCAL
                                                                                                                         514 DLVPLIDGSGSIGSYVFKNEVLRFVREFVELFBIGRSKTRVGLIQYSDQIRHEFDLDQYG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 LNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 ----VIIALTDGELHEDLFFYSEREANRSRDLGAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 ERSQ-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1; 492/3; 53 The proenzyme forms a complex with C4a and is activated by cleavage into C2a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYB------NRQGYRTAS- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53,
                                                                                                                                                                                     4 DLYFILDKSGSVLHH--WNEIYYFVEQLAHKFI--SPQLRMSFIVFSTRGTTLMKLTE--
                                                                                                                                                                                                                                                          55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE 57
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
DRDSLLKGISETQ-YLTGLTRTGAAIQHMVQEGF-----SERRGARPQQSDIARVA
                                                           DREQIRQGLEELQKVLPG----GDTYMH---EGFERASEQIYYENRQGYR-----TASVI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILS
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                 12.0%; Score 116; DB 2; 28.2%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2%; Score 118.5; DB 24.4%; Pred. No. 0.029;
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                                                                                                                              Length 3051;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VYCVGV-----KD 142
                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                           57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
   623
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F;40-204/Domain: von Willebrand factor type A repeat homology F;336-317/Domain: fibronectin type III repeat homology <FN3A> F;336-409/Domain: fibronectin type III repeat homology <FN3B> F;418-498/Domain: fibronectin type III repeat homology <FN3C> F;507-591/Domain: fibronectin type III repeat homology <FN3D> F;625-707/Domain: fibronectin type III repeat homology <FN3D> F;625-707/Domain: fibronectin type III repeat homology <FN3D>
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C;Species: Gallus gallus (chicken)
C;Species: To-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Date: 10-Sep-1999 #text_change
C;Date: 10-Sep-1999 #text_change
C;Date: 10-Sep-1999 #text_change
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C;Date: 10-
                                                                                                                                                                                                                                                                                                     F;716-798/Domain: fibronectin type III repeat homology <RN3F>F;806-893/Domain: fibronectin type III repeat homology <FN3G>F;804-1089/Domain: von Willebrand factor type A repeat homology F;1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1551-1570; 1593-1599; 1639-1667 < GOR2 > C; Keywords: alternative splicing; coiled coil; es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, Bur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
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A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide translation
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A; Residues: 1472-1659 <GORl>
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Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
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A;Reference number: S30085
A;Accession: S30085
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A;Residues: 1472-1660 <APT>
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                                                                                                                                                                                                                                                 F;1554-1659/Domain: triple helical domain COL1 #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: S20833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                 Query Match
Best Local
                                                                 Local Similarity
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                                                          11.6%;
39;
                                                          Score 113; DB 2;
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coiled coil; extracellular matrix; glycoprotein; trime:
      Mismatches
      8O;
                                                                                                                           Length 1747;
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20;
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Gaps
      11;
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DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 57

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C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycopro F;1-28/Domain: signal sequence #status predicted <SIG>F;2-98/Domain: signal sequence #status predicted <SIG>F;29-10/Domain: fibronectin type III repeat homology <FNJA>F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>F;156-320/Domain: fibronectin type III repeat homology <FNJB>F;442-525/Domain: fibronectin type III repeat homology <FNJS>F;54-614/Domain: fibronectin type III repeat homology <FNJS>F;531-707/Domain: fibronectin type III repeat homology <FNJS>F;631-707/Domain: fibronectin type III repeat homology <FNJSP>F;632-914/Domain: fibronectin type III repeat homology <FNJSP>F;941-823/Domain: fibronectin type III repeat homology <FNJSP>F;941-823/Domain: fibronectin type III repeat homology <FNJSP>F;942-1009/Domain: fibronectin type III repeat homology <FNJSP>F;922-1009/Domain: fibronectin type III repeat homology <FNJSP>F;1040-1205/Domain: fibronectin type III repeat homology <FNJSP>FIBRONECTIN type III re
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C;Date: 11-Mar-
C;Accession: S3
R;Waelchli, C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
S31212
    collagen alpha 1(XIV) chain precursor,
C;Species: Gallus gallus (chicken)
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
                                                                                    S78476
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A; Residues: 1-1857 <WAE>
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                                                                                                                    RESULT 11
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gallus
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26.1%; Pred. No. 0.25;
tive 39; Mismatches 80; Indels 2
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                                        form
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to the EMBL Data Library, January 1993
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                                        chicken
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F;39-110/Domain: fibronectin type III repeat homology <FN3F>
F;35-43/Domain: fibronectin type III repeat homology <FN3F>
F;442-525/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;434-614/Domain: fibronectin type III repeat homology <FN3E>
F;633-707/Domain: fibronectin type III repeat homology <FN3F>
F;623-707/Domain: fibronectin type III repeat homology <FN3F>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F,832-914/Domain: fibronectin type III repeat homology <FN3F>
F,922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
BBHU
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A;Residues: 1-416;1460-1811,1843-1888
A;Cross-references: EMBL:X70793
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A; Cross-references: UNIPROT: P32018;
R; Waelchli, C.; Trueb, J.; Kessler,
Eur. J. Biochem. 212, 483-490, 1993
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                                                                                                             문
                        RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;
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                                                                                                             1213 DELITFVC 1220
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49; Conserv
                                                                                                                                                                       HSILKKSC 180
                                                                                                                                                                                                                                                                                     DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 172
                                                                                                                                                                                                                                                                                                                                                                                                      DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
                                                                                                                                                                                                                                 DV-----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%;
ilarity 26.1%;
Conservative 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 113; DB
Pred. No. 0.25;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL:X70793; NID:g288872; PIDN:CAA50064.1; PID:g28887
B.; Winterhalter, K.H.; Trueb, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              form #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                  1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trimer
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complement factor B precursor [validated] - human ; Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-ly; Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment C; Species: Homo sapiens (man) C; Date: 19-Feb-1984 #sequence\_revision 05-Aug-1994 #text\_change 09-Jul-2004 C; Accession: S34075; A44628; A0934; A19188; A19947; B19947; B25971; S14339; A44628; I544 R; Mejla, J.E.; Jahn, J.; de la Salle, H.; Hauptmann, G. R; Mejla, J.S.; Jahn, J.; de la Salle, H.; Hauptmann, G. A; Reference number: S34075

A;Cross-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN:CAA51389.1; R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R. Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein factor B, a

PID:g2975

A;Reference number: S34
A;Accession: S34075
A;Molecule type: mRNA
A;Residues: 1-764 <MEJ>

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A; Molecule type: protein
A; Residues: 270-329 «NIE»
A; Note: binding site for carbohydrate to lysine
R; Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-99 <WUL>
A;Residues: 1-99 <WUL>
A;Residues: 1-99 <WUL>
A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
A;Niemann, M.A.; Bhown, A.S.; Miller, E.J.
Blochem, J. 274, 473-480, 1991
Blochem, J. 274, 473-480, 1991
A;Title: The principal site of glycation of human complement
A;Reference number: S14339; MUID:91174758; PMID:2006911
A;Accession: S14339
                                                                                                                                                                                                                                                       A;Molecule type: mRNA,
A;Residues: 16-225, 'F, '27-259 <MOR>
A;Residues: 16-225, 'F, '27-259 <MOR>
R;Residues: 16-225, 'F, '27-259 <MOR>
R;Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties of a recombinant zymogen of th A;Reference number: I54409; MUID:94041399; PMID:8225386
A;Accession: I54409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Internal homologies of the Ba fragment from human A;Reference number: A44628; MUID:84158524; PMID:6323161 A;Accession: A44628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 339-509 <CA1>
A;Residues: 339-509 <CA1>
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
R;Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human complement protein factor B gene: evidence A;Reference number: A25971; MUID:87102880; PMID:3643061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. J. 209, 61-70, 1983
A/Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of A/Reference number: A19188; MUID:83204002; PMID:6342610
A/Contents: the final paper in a series documenting the sequence, glycosylation site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Cross-references: GB:J00185; GB:J00186
A/Note: the authors translated the codon TAC at 519 as Thr; t
R/MOle, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.B.
J. Biol. Chem. 259, 3407-3412, 1984
A/Title: Complete primary structure for the zymogen of human
A/Reference number: A20751; MUID:84161997; PMID:6546754
                   A;Residues: 1-764 <RES>
A;Residues: 1-764 <RES>
A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689
A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689
A;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Pujita, S.; Volanakis,
Mol. Immunol. 30, 1587-1592, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Campbell, R.D.; Porter, R.R. 80, 4464-4468, 1983 Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983 A;Title: Molecular cloning and characterization of the A;Reference number: A19947; MUID:83273641; PMID:6308626
                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-764 < RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A/Residues: 339-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 467-546; 550-595; 752-764 < WOO>
                                                                                                                                                                                                                         A,Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: B25971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 346-764 < CAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: protein
A, Residues: 260-296, 'T', 298-764 <CHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Note: glycosylation sites were determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: nucleic acid translation differs from A;Note: 736-Ser was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein; mRNA
A; Residues: 26-764 < MOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Christie, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L.; Gagnon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                         GB/EMBL/DDBJ
cDNA cloning, nucleotide sequencing, phenotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMID:6957884
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                                                                        J.B.
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conv
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C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; v C;Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrol P;1-25/Domain: signal sequence #status predicted <SIG> F;26-764/Product: complement factor B #status experimental <MAT> F;26-259/Product: complement factor B #status experimental <BAF> F;37-98/Domain: complement factor H repeat homology <FH1> F;103-158/Domain: complement factor H repeat homology <FH2> F;105-218/Domain: complement factor H repeat homology <FH3> F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF> F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF> F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF> F;260-764/Domain: von Willebrand factor type A repeat homology <VFA> F;482-752/Domain: trypsin homology #status atypical <TRY> F;37-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Di F;122,142,285,378/Binding site: carbohydrate (Asn) (covalent) #status experimental F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental F;550-560,576,699/Active site: His, Asp, Ser #status experimental
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C;Superfami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor C3/C5 convertase; Ba is released
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A;Molecule type: mRNA
A;Residues: 1-31, (2, 33-764 <RE2>
A;Cross-references: GB:L15702; NID:g29:
C;Comment: 292-Cys has a free sulfhydry
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
439 INALASKKDNEQHVFKVKD-MENLEDVFYQMIDES 472
                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                 325 SEADSSNADWVTKQLNEINYEDHKLKSGTNT-----KKALQAVYSMMSWPDDVPPEGWN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                    ETQLARIADSKDHVFPVNDGFQALQGIIHSILKKS 179
                                                                                                                                                                                                                                                                                                                                                                                                                       GSMNIYLVLDGSDSIGASNFTGAKKCLVNLIEKVASYGVKP--RYGLVTYATYPKIWVKV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGFDLYFILDKSGSV-----LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKL 55
                                                                                                                                        RTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPREDYLDVYVFGVGPLVNQVN 438
                                                                                                                                                                                                  RTASVIIALTDG-----
                                                                                                                                                                                                                                                                                                                                                  TB----DREQIRQGLEEL----QKVLPGGDTYMHEGFERASEQIYYENR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111.5; DI
Pred. No. 0.11;
4; Mismatches
                                                                                                                                                                                                         ----ELHEDLFFYSEREANRSRDLGAIVYCVG--VKDFN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMID:8247029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele
A;Reference number: I51027; MUID:95246925; PMID:7729585
A;Accession: I51027
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                 type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
A;Cross-references: UNIPROT:Q91145; EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g63264
F;155-236/Domain: fibronectin type III repeat homology <3FR>
                                                                                             A; Molecule type:
                                                                                                                                                                                                                                                                                                                            C;Accession: I51027
                                                                  A; Residues: 1-929 <WEI>
                                                                                                                              A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                   Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                   mRNA
                                                                                                                                 from GB/EMBL/DDBJ
                                                                                                                                                                                                                           alpha
                                                                                                                                                                                                                               chain
                                                                                                                                                                                                                           of type XII collage
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Collagen alpha 1 (VII) chain precursor - human

W.Alternate names: procollagen alpha 1 (VII) chain

C.Species: Nomo sapiens (man)

C.Species: Nomo sapiens (man)

C.Species: Nomo sapiens (man)

C.Species: Nomo sapiens (man)

C.Species: Nomo sapiens (man)

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C.Species: Nomo sapiens (man)

R.Species: Nomo sapiens (man)

R.Species: Nomo sapiens (man)

R.Species: Commission (man)

A.Statis: not compared with conceptual translation

A.Scelius: not compared with conceptual translation

A.Scelius: not compared with conceptual translation

A.Scelius: Nomo sapiens (man)

A.Scelius: Nomo sapiens (man)

A.Scelius: Nomo sapiens (man)

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A.Scelius: Nomo sapiens (man)

A.Scelius: Nomo sapiens
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N;Alternate names: procollagen alpha 1(VII) chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750 IVAPSKRYA----DEGIELYAVGIKNADENELKEIASDPDELYMYNVADFSLLTNIVNDL
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Similarity 23.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD
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  protein
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A;Contents: annotation
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                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
  174
                                                    154
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F;1170-1172/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cysteine/proline-rich
F;1254-2783/Region: interrupted helical
F;1334-1336/Region: cell attachment (R-G-D) motif
F;1334-1336/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2753-2555/Region: cell attachment (R-G-D) motif
F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;337,786,1109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;3167,2176,2185,2189,2664,2667,2673/Modified site: 4-hydroxypyroline
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;231-318/Domain: fibronectin type III repeat homology e;327-413/Domain: fibronectin type III repeat homology e;414-502/Domain: fibronectin type III repeat homology e;508-593/Domain: fibronectin type III repeat homology e;598-683/Domain: fibronectin type III repeat homology e;598-683/Domain: fibronectin type III repeat homology e;7686-771/Domain: fibronectin type III repeat homology e;76-862/Domain: fibronectin type III repeat homology e;864-952/Domain: fibronectin type III repeat homology e;954-1045/Domain: fibronectin type III
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A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys: A;Note: there are 118 introns
C;Complex: type VII collarer in number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolir F;1-16/Domain: signal sequence #status predicted <SIG>F;17-2944/product: collagen alpha 1(VII) chain #status predicted <MAT>F;17-1253/Domain: amino-terminal nonhelical #attus predicted <MAT>
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R;Christiano, A.M.; Ryymaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly
A;Reference number: A55255; MUID:94224777; PMID:8170945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 2, 273-278, 1993
A;Title: The carboxyl-terminal half of type VII collagen,
A;Reference number: I48103; MUID:93271985; PMID:8499916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C_iComment: Prolines and lysines at the third position of the tripeptide repeating ed and subsequently O-glycosylated.
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A; Residues: 2395-2871, 'S', 2873-2944 <RE2>
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                                                                                                       116 DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH
                                                                                                                                                                                                                     98 GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                                                                                                                                       56 TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                38 DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
DLV---DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVND-FSILRTLLP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.3%; Score 110; DB 2; Length 2944; 26.2%; Pred. No. 0.78;
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repeat homology <FN2>
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t homology <FN4>
t homology <FN5>
t homology <FN6>
t homology <FN6>
t homology <FN7>
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A;Molecule type: mRNA
A;Residues: 266-267;/S', 269-294,'L',296-600 < CON>
A;Residues: 266-267;/S', 269-294,'L',296-600 < CON>
A;Residues: 266-267;/S', 269-294,'L',296-600 < CON>
A;Residues: 266-267;/S', 269-294,'L',296-600 < CON>
A;Residues: 266-267;/S', 269-267]
A;Cross-references: GB:L06343; NID:g192671; PIDN:AAA37441.1; PID:g192672
A;Ross-references: GB:L06343; NID:g192671; PIDN:AAA37441.1; PID:g192672
A;Note: the sequence from Pig. 3 is inconsistent type A repeat homology
C;Keywords: alternative splicing; cartilage; cell binding; connective tissue; disulfide
F;128-Domain: collagen alpha 2(VI) chain #status predicted <NICs-
F;29-1029/Product: collagen alpha 2(VI) chain #status predicted <NICs-
F;29-265/Domain: globular #status predicted <NICs-
F;246-226/Domain: collagenous #status predicted <NICs-
F;366-600/Domain: collagenous #status predicted <NICs-
F;366-38/Region: cell attachment (R-G-D) motif
F;499-501/Region: cell attachment (R-G-D) motif
F;508-51/Region: cell attachment (R-G-D) motif
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A;Residues: 1-1029 <IBR>
A;Residues: 1-1029 <IBR>
A;Crose-references: UNIPROT: (002788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49808
A;Crose-references: UNIPROT: (002788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49808
A;Crose-references: UniproT: (002788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49808
B;Crose-references: UniproT: (002788)
Biochem. J. 289, 141-147, 1993
Biochem. J. 289, 141-147, 1993
A;Title: Cloning of alpha2 chain of type VI collagen and expression during mouse develop A;Reference number: S28808; MUID:93143659; PMID:8380980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C/Species: Mus musculus (house mouse)
C/Spate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S21369; S28808; S133745; S18863
R/Ibrahlmi, X.Y.Z.; Bardon, X.Y.Z.; Dani, C.
submitted to the EMBL Data Library, April 1992
A/Reference number: S21369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;601-1029/Domain: globular #status predicted <NC1>
F;623-799/Domain: von Willebrand factor type A repeat homology <VWA2>
F;841-1012/Domain: von Willebrand factor type A repeat homology <VWA3>
F;841-1012/Domain: von Willebrand factor type A repeat homology <VWA3>
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A,Accession: $13745
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A, Residues: 266-1029 < IB2>
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                                                                               163
                                                                                                                                                                                                                                              110 DGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVN----- 162
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Similarity 23.5%;
DSTEIDODTINRIIKVMKHEAYGECYKVSCLEI 264
                                                                               DGFQALQGIIHSIL------KKSCIEI 183
                                                                                                                                                               DGHVTGSPCGGIKMQAERAREEGIRLFALAPNRNLNEQGLRDIANSPHELYRNNYATMRP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVYFVLDTSESVAMQSPTDSLLYHMQQFVPQFISQLQNEFYLDQVALSWRYGGLHFSDQV 115
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Q70350
Q28984
CO2 MOUSE
Q8CBT2
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Q9ES77
Q75R52
                                                                                                                                                            ITAX HUMAN
ITAM MOUSE
ITAD HUMAN
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O9cz52 mus musčulu P58335 homo sapien O6dfxz mus musculu O8bym2 mus musculu O8bym2 mus musculu O9byg8 halocynthia O9gye7 rattus norv O8t5c3 mytilus edu O60847 mus musculu O8t5c2 mytilus gal O04588 eimeria max P11215 homo sapien O99715 homo sapien O99715 homo sapien O9089 mus musculu P13944 gallus gall O43981 eimeria ten O9u89 neospora ca O43853 homo sapien P20702 homo sapien P20702 homo sapien P20703 mus musculu O13349 homo sapien P05555 mus musculu O13349 homo sapien P05550 mus musculu O28984 sus scrofa P21180 mus musculu O8cbt2 mus musculu O8cbt2 mus musculu O8cbt2 mus musculu O7prp5 anopheles g O9es77 mus musculu O7prp5 anopheles g O9es77 mus musculu O7prp5 anopheles g O9es77 mus musculu O7prp5 anopheles g
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Q9cz52 mus musculu
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112	112.5	112.5	113	113	113.5	114.5	114.5	116	116	116	116	116	116
11.5	11.6	11.6	11.6	11.6	11.7	11.8	11.8	12.0	12.0	12.0	12.0	12.0	12.0
588	1034	337	1888	599	790	2104	2104	3767	3183	2944	1329	1284	637
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Q6ZED8	Q8K229	Q8C972	CA1E_CHICK	QBMVQ1	Q6DCQ6	Q964N4	Q21281	MUA3_CAEEL	Q65ZC2	Q63870	KF10_HUMAN	Q6PIS9	QBIVX1
Q6zed8 synechocyst	Q8k229 mus musculu	Q8c972 mus musculu	P32018 gallus gall				Q21281 caenorhabdi			mus n	homo	homo	Q8ivxl homo sapien

# ALIGNMENTS

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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
Hillman R.T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
-!- FUNCTION: Cellular role is not yet known.
-!- SUBNUIT: Binds to the protective antigen (PA) of Bacillus anthracis. Binding does not occur in the presence of calcinosus anthracis. Binding does not occur in the presence of calcinosus anthracis. Binding does not occur in the presence of calcinosus anthracis. Binding does not occur in the presence of calcinosus anthracis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100; Scoble H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNAB
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                                                                                                                                             - TISSUE SPECIFICITY: I but not in normal end to but not in normal end - DOMAIN: Behongs to SIMILARITY: Belongs to SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=4; Comment=Experimental confirmation may be law
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences.";
                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                             IsoId=Q9H6X2-4;
                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9H6X2-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9H6X2-2; Sequence=VSP_000444,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad.
                                                                                                                                         SPECIFICITY: Highly expressed in tumor endothelial of in normal endothelial cells.

Binding to PA seems to be effected through the VWA
ITY: Belongs to the ATR family.

ITY: Contains 1 VWFA domain.
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Swiss Institut
Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence=VSP_000446,
                                                                                                                                                                                                                                                                                                                                         Sequence=VSP_000448,
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Best Local :
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PF05587; Anth Ig; I.
Pfam; PF05586; Anth C; 1.
Pfam; PF00092; VWA; 1.
SMART; SM00327; VWA; 1.
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AF421380;
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                                                                                                                                                                                                                                                                                                                 Similarity
IEILAAE
                                                                                              SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                                                                                                    QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                                                                                                       GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
                                                                                                                                                                                                                                             GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
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AAL26496.1;
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BAA91707.1;
AAH12074.1;
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Cytoplasmic (Potential)
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Pred. No. 2.1e-74;
; Mismatches 0;
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RESULT 2 ATR1\_MOUSE ID ATR1\_MOUSE

STANDARD;

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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Sato K.,
RA Shizaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Yoshino M., Waterston R., Lander S.S., Rogers J.,
RA Yasunishi A., Kohasi Y., Tangara Based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CZ52;
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Createu,
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Anthrax toxin receptor 1 precursor (Tumor endothelial marker
Anthrax toxin synonyms=Atr, Tem8;
                                   modified
                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the companies of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60,770 full-length cDNAs ";
Nature 420:563-573(2002).
-i- FUNCTION: Cellular role is not yet known.
-i- SUBUNIT: Binds to the protective antigen (PA)
anthracis (By similarity).
-i- SUBCELLULAR LOCATION: Type I membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Res. 61:6649-6655(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of the mouse transcriptome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cell surface tumor endothelial markers
                            ween the Swise Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: Event=Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9CZ52-1;
                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9CZ52-2; Sequence=VSP_000450;
                                                                                                                                                                                                                                                                                                                Bimilarity
and this statement is not removed. Usage by and for commercia. requires a license agreement (See http://www.isb-sib.ch/announce.
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                                                                                                                                                                                                                                                                                                                                         Binding to
                                                                                                                                                                                                                                                                                                                                                                                experimental
                                                                                                                                                                                                                                        Belongs to
Contains 1
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                                                                                                                                                                                                                                        VWFA
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                                                                                                                                                                                                                                        domain.
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Best Local
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PF05587; Anth Ig; I.
Pfam; PF05586; Anth Ig; I.
Pfam; PF00506; Anth Ig; I.
Pfam; PF0092; VWA; I.
PROSITE; P850234; VWFA; I.
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TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                            ATR2 HUMAN STANDARD; PRT; 489 AA P58335; Q86UI1; Q8NB13; Q96NC7; 28-FBB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation updat Anthrax toxin receptor 2 precursor (Capilla
                                                                                                                                                                                                                    HUMAN
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VARSPLIC
Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.A., Davis G.E.;
"Differential gene expression during capillary morphogenesis collagen matrices: regulated expression of genes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                            MEDLINE=21539596;
                                                                                                               Homo sapiens
                                                                                                                          Name=ANTXR2; Synonyms=CMG2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK013005; BAB28591
MGD; MGI:1916788; Antxrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                        SEQUENCE FROM N.A.
                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                            159
                                                                                                                                                                                                                                                                219
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                                                                                                                                                                                                                                                                                                                                                                                                               GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
                                                                                                                                                                                                                                                                                                                         SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                                                                                                                                                                                                                                                                                      QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENSQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                                                                                                                                                                                                                                                                                    GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHRFISPQLRMSFIVFSTRGTTLMKLTEDRE
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                                                                                                              (Human)
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                                            PubMed=11683410;
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319
340
562
213
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182
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                                                        (ISOFORM
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                                                                                                     Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW.;
                                                         2)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 961; DB 1;
Pred. No. 1.2e-73
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA
WMFSSFLERAFQ (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asp/Glu-rich
Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anthrax toxin receptor Extracellular (Potentia
                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6AC92049B4BB4F7C CRC64;
                                                                                                                                               ion update)
(Capillary
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basement
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa E.,
RA Tishida S., Ono Y., Takiguchi S., Wattanabe S., Yosida M., Hotuta T.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki M., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takama S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Mishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Monoriya S., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Matsumura K., Nakajina Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Masaho Y., Nakagawa K.,
RA Nakajara F., Namura N., Kikuchi H., Masaho Y., Yamashita R.,
RA Nakajara T., Namura N., Kikuchi H., Masaho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT Complete sequencing and characterization of 21,243 full-length human
   +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100; Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane matrix assembly, cell cycle progression, differentiation and G-protein signaling.";
J. Cell Sci. 114:2755-2773(2001).
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PubMed=14702039; DOI=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Cellular role is not yet known. (PA) of Bacillus SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the following preference: calcium - manganese - magnesium - zinc. Seems to bind to collagen type IV and laminin. SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmic
liver, peripheral blood leuk
small intestine and spleen.
DOMAIN: Binding to PA seems
SIMILARITY: Belongs to the A
                                                                                                                      Note=No experimental TISSUE SPECIFICITY: Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Experimental Exp
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                                                                                                                                                                                      IsoId=P58335-4; Sequence=VSP_008346;
                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P58335-1;
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                                                                                         peripheral blood leukocytes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36:40-45(2004).
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                                                                                                                                                                                                                                                  experimental
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                                                                                                                                                                                                                                               Sequence=VSP_008344, VSP_008
ental confirmation available;
                                                                                                                                                                                                                                                                                                                                  Sequence=VSP_008343;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; Named isoforms=4;
                                                                                                                      Expressed in colon, heart,
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                            through the VWA domain
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                                                                                         skeletal
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or send a
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                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                   RQGLBELQKYLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSE
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                                                                                                                                                                                                              FDLYFVLDKSGSVANNWIEIYNFVQQLAERFVSPEMRLSFIVFSSQATIILPLTGDRGKI
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AAP04016.1;
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TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI
VTQAGVKWHDLTHCTFGLSGSGDPPTSAS (in
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P -> A (in Ref. 3;
B9F679DB75B6E2B7
                                                PRT;
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A Strausborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Wedin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

A Korywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Kornes G. T. Maxra M. A., Schmutz J., Myers R.M., Schein J.E.,

Kornes G. T. Maxra M. A., Schmutz J., Myers R.M., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 109
  Q8BVM2,
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InterPro;
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MEDLINE=22388257;
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CTDAIN=C57BL/6; TISSUE=Eye;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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arPro; IPR008399; Ant C.
arPro; IPR002035; VWF A.
n; PP05587; Anth Ig; I.
n; PP05586; Ant C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
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Pred. No. 2e-38;
2; Mismatches
                       PRT;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carminci p., Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/65; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yokazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;

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Genome Res. 10:1757-1771(2000).
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STRAIN-C57BL/6J; TISSUE-Testis;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

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Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical proline-rich reg:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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SEQUENCE FROM N.A.
TISSUE=Testis;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Mammalia; Eutheria;
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BAC36683.1;
C:integral (
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Rodentia;
   to membrane;
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Sciurognathi; Muridae;
   IEA
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on functional
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, Sano H.,
v . Tagami /
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Best Local s
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GO; GO:0016021; C:integral to membrane
GO; GO:0008305; C:integrin complex; IE
GO; GO:0005515; F:protein binding; IEA
GO; GO:0007160; F:cell-matrix adhesion
GO; GO:0007229; F:integrin-mediated si
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; WMF A.

Pfam; PF00092; VWA; 1.
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01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning
                  Cell adhesion;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
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Pfam; PF00092; VWA; I.
PRINTS; PR00452; VWPADOMAIN.
SWART; SW00327; VWA; I.
PROSITE; PS50234; VWFA; I.
                                             PROSITE; PS50234; VWFA; 1.
Cell adhesion; Integrin; Signal; Transmembrane.
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01-UN-2001 (TYEMBLrel. 17, Last sequence update)
01-UN-2003 (TYEMBLrel. 24, Last annotation update)
Integrin alpha Hrl precursor.
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InterPro; IPR002035; VWF_A.
                                                                                                                                                   PRINTS; PR01185; INTEGRINA. PRINTS; PR00453; VWFADOMAIN.
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MEDLINE=21103187; PubMed=11160215;
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- SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                                                           GO:0016021; C:integral to membrane; IEA.
GO:0008305; C:integrin complex; IEA.
GO:0005515; F:protein binding; IEA.
GO:0007160; P:cell-matrix adhesion; IEA.
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                                                                                                  SM00191; Int_alpha; 5.
SM00327; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Azumi K., Nonaka M.;
and characterization of integrin alpha
ascidian, Halocynthia roretzi.";
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Rattus norvegicus (Rat)
Enkarvota; Metazoa; Chordata;
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                                                     EMBL; AF021334; AAF21241.1; -. HSSP; P11215; 1BHQ.
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O'Brien M.M., VanderVieren M., Kilgannon P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                          InterPro; IPR000413; InterPro; IPR002035;
                                                                                                                                                                                                        entities requires a license agreement
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PRINTS;
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             PF01839; FG-GAP;
PF00357; Integrin
PF00092; VWA; 1.
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OBT6U5;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1 variant a.
Mytilus edulis (Blue mussel).
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PROSITE; PS50234; VWFA; 1.
Calcium; Cell_adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
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SM00327; VWA; 1.
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SM00191; Int_alpha; 5.
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FG-GAP 5.
FG-GAP 6.
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Extracellular (Potential).
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Best Local :
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;

"Collagen-binding matrix proteins from elastomeric extrace byssal fibers.";
                                                        SEQUENCE
                                                                 PRINTS; PR00453; VWFADOMAIN
SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
Matrix protein.
                                                                                                                                   EMBL; AY053390; AAL17973.1; -.
GO; GO:0005198; F:structural molecule activity; IEA
InterPro; IPRO20335; VWF_A.
                                                                                                                                                                                                                                                                                              Mytilus edulis (Blue mussel).
Bukaryota; Metazoa; Mollusca; Bivalvia;
Mytiloidea; Mytilidae; Mytilus.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
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EMBL; AF414454; AAL83537.1; -.
GO; GO:0005198; F:structural molecul
InterPro; IPRO2035; VWF_A.
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;
                                                                                                                                                                                                                                                                                                                                       Proximal thread matrix protein 1b.
                                                                                                                                                                                                                                                                                                                                                                                              Q8T5C3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                          Pfam; PF00092; VWA;
                                                                                                                                                                                  Biomacromolecules 3:1240-1248(2002).
                                                                                                                                                                                                                                                                               NCBI_TaxID=6550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFFVND 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLTE--DREQIRQGLEELQKVLPG--GDTYMHEGFERASEQIYYENRQG---YRTASVII 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGFDLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLM
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                                                      444 AA;
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Score 141; DB
Pred. No. 0.00
46; Mismatches
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Pred. No. 0.001;
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O60847; P70332;
15-JUL-1998 (Rel. 36, C
28-PEB-2003 (Rel. 41, L
25-OCT-2004 (Rel. 45, L
COllagen alpha 1(XII)
Name=COll2a1;
Name=COll2a1;
                                                                                                                               Dev.
                                                                                                                                                                                                                                                                                      MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants
collagen XII and their tissue-specific expression during
development.";
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                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J,
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                 MEDLINE=99348349; PubMed=10419532; DOI=10.1074/jbc.274.31.22053;
                                                                                                                                                                                                                                                           PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                    development
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                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
IsoId=Q60847-4; Sequence=VSP_001150, VSP_001151, VSTISSUE SPECIFICITY: Highest expression in tendons, poskin, cornea, sclera, blood vessels, and periosteum. DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are pearly stages (ED7 and 11); at later stages of developments.
                                                                                                  Event-Alternative splicing; Named isoforms=4;
Comment=The final tissue form of collagen XII
homotrimers or any combination of the various
                                                                                 Name=XIIA-1; Sequence=Displayed; IsoId=Q60847-1; Sequence=Displayed;
                                                                                                                              nontriple-helical seq
ALTERNATIVE PRODUCTS:
                                           Name=XIIB-2
                                                                  Name=XIIA-2; Synonyms=ER#K;
IsoId=Q60847-2; Sequence=
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                                                   IsoId=Q60847-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LITDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTS
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                                                                                                                                                                                                                                                         FROM N.A.,
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                                                 Sequence=VSP_001150;
                                                                Sequence=VSP_001151,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     chain precursor.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                          ALTERNATIVE
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                                                                  VSP_001152
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 development
       are predominant
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murinae; Mus.
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                       VSP_001152;
perichondrium,
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and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice varial continues to be expressed in several tissues, even after birth. The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages o embryonic development (ED15 and ED17).
                                                                                                                                                                                                                                                   variant
at
                                                                                    Of
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PTM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).

PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By

unit (G-X-Y) are hydroxytated in some or all or the similarity).
similarity).
PTM: O-glycosylation of isoform XIIA-2; glycosaminoglycan of (G-X-Y) are hydroxylated

chondroitin-sulfate type (By similarity).
SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family.
SIMILARITY: Contains 18 fibronectin type III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWFA domains. collagens

domains.

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MGD; MGI:88448; Coll2al.
InterPro; IPR008160; Collagen.
InterPro; IPR008985; ConA\_like\_lec\_
InterPro; IPR008985; FN\_III.
InterPro; IPR008957; FN\_III-like.
InterPro; IPR003129; TSP\_N.
InterPro; IPR003129; VWF\_A.
Pfam; PF01391; Collagen; 5.
Pfam; PF00041; fn3; 18. PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00260; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; VWFA; 4. Alternative PF00041; fn3; 1: PF02210; TSP N; PF00092; VWA; 4 splicing; Cell adhesion; Collagen;
n; Hydroxylation; Repeat; Signal; St \_like\_lec\_ 91.

Glycoprotein; SIGNAL Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin Fibronectin VWFA 1. Fibronectin VWFA VWFA 2. Collagen alpha 1(XII) chain Potential. u. type-III type-III type-III type-III type-III type-III type-III type-III
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type-III type-III type-III Structural Extracellular matrix; 10. 12. 13. 14. 15. 17. ۲. ø 8 7 6 5 4 9 protein

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TSP N-terminal.
Nonhelical region
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Pred. No. 0.015;
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7; Mismatches
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Missing (In isoform XIIA-2
XIIB-2).
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MEDLINE=93149203; PubMed=8426611; DOI=10.1016/0166-6851(93)90255-V; Pasamontes L.E., Hug D., Huembelin M., Weber G.; "Sequence of a major Eimeria maxima antigen homologous to the Eimericenella microneme protein Etpl00."; Mol. Biochem. Parasitol. 57:171-174(1993). EMBL; M99058; AAA29076.1; -... EMBL; M99058; AAA29076.1; -... ERGE; A48569; A48569. HSSP; P07996; ILSL. GO; GO:0008083; F:growth factor activity; IEA. InterPro; IPR000762; PTN MK.
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01.-JUN-2002 (TrEMBLrel. 21, Created)
01.-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01.-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01.-JUN-2003 (TrEMBLrel. 24, Last annotation update)
proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                         004588;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00327; VWA; 2.
PROSITE; PR50234; VWFA; 2.
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HSSP; P20701; 1MJN.
GO; GO:0005198; F:structura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903. Sun C., Lucas J.M., Waite J.H.; "Collagen-binding matrix proteins from elastomeric extrac byssal fibers.";
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                      Major antigen homologous
Eimeria maxima.
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Pfam; PF00092; VWA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVND
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; Pred. No. 0.00
44; Mismatches
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Pfam; PF00092; VWA; 1.

PRINTS; PR00453; UWPADOMAIN.

SMART; SM00209; TSP1; 6.

SMART; SM00327; UWA; 1.

PROSITE; PS50092; TSP1; 5.

PROSITE; PS50092; TSP1; 5.

PROSITE; PS50234; UWFA; 1.

SEQUENCE 724 AA; 75808 MW;
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01-JUL-1989
01-OCT-1996
                                                                                                                                                        MEDLINE-88257215; PubMed=2454931; DOI=1
SEQUENCE FROM N.A. MEDLINE=93123748; Fleming J.C., Pahl
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01-JUL-1989 (Rel. 34, Last sequence update)
01-CCT-2994 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor Neutrophil adherence receptor).
Name=ITGAM; Synonyms=CD11B, CR3A;
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Mammalia; Eutheria;
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l H.L., Gonzalez
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Primates;
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"Experimental support for a beta-propeller domain in integrin alpha-
subunits and a calcium binding site on its lower surface.";
Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).

-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles
It is identical with CR-3, the receptor for the iC3b fragment of
the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
of fibrinogen gamma chain.
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                                                                                                                                                                                               3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195;
Oxvig C., Springer T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
MEDLINE=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shelley C.S., Arnaout M.A.;
"The promoter of the CD11b gene directs developmentally regulated expression.";
proc. Natl. Acad. Sci. U.S.A. 88:10525-1
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                                                                                                                                                                                                                                                                      Structure
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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8; Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Brairbanks M.B., Finzel B.C., Garlick R.L., Heinriks R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation?"
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MEDLLNE=96363671; PubMed=8747460; DOL=10.016/S0969-2126(01)00271-4;
Lee J.O., Banketon L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway fo:
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                                                                                                                                                                                                                                                                                                       Kelley L.L., Mildner A.M., Moon J.B., Mott ., Tomich C.S., Watenpaugh K.D., Wiley V.H.; ing to the integrin CD11b I domain and activ
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Hickey M.J., Ozols
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S.A. 88:10525-10529(1991)
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MIM; 120980; -.
GO; GO:0008305; C:integrin complex;
GO; GO:0007155; P:cell adhesion; TA:
InterPro; IPR000413; Integrin_alpha
InterPro; IPR002035; VWF_A.
                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain fami
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdilb.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granulocytes DOMAIN: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M associates with beta-2. SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                  1BHO,
1BHO,
1IDO,
1JLM,
                                                                                                                                                                                                                                                                                           A31108;
1A8X; Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S52157;
S52159;
S52161;
S52164;
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S52154; AAB24821.1;
                                                                                                          HGNC: 6149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See http:\overline{//www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                       X-ray; @=140-331.

X-ray; @=143-334.

X-ray; A=137-331.

X-ray; A=144-337.

X-ray; A=144-335.

X-ray; A=144-345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB24821.1; JOI
AAB24821.1; JOI
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X-ray; 1/2=-.
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AAB24821
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AAB24821.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration - MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Integrine
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RESULT 14
CA1C_HUMAN
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                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.

MEDLINE-97288521; PubMed-9143499; DOI=10.1006/geno.1997.4638;

WAS Gerecke D.R., Olson P.F., Knoll J.H.M., Taylor R.\

Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.;

"Complete primary structure of two splice variants of collagen XII,

and assignment of alpha 1(XII) collagen (CCL12A1), alpha 1(X)

collagen (CCL9A1), and alpha 1(XIX) collagen (CCL19A1) to human

chromosome 6q12-q13.";

Genomics 41:336-242(1997).

Genomics 41:336-242(1997).

Genomics 41:336-242(1997).

Genomics 41:336-242(1997).

Genomics 41:336-242(1997).

Genomics 41:336-242(1997).

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Genomics 4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     099715; Q99716;
15-JUL-1998 (Rel. 36, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
25-OCT-2004 (Rel. 45, Last annotation
Collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOWAIN.
SWART; SW00191; Int_alpha; 5.
SWART; SW00191; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
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PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct
                                                                                                                                                                +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA1C_HUMAN
                                                                ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or an
combination of isoform Long and isoform Short;
                Name=Long;
IsoId=Q99715-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315
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PF00357; Integrin_alpha;
PF00092; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTFKEFONNPNPRSLVKPITOLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.7%;
                        Sequence=Displayed,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 132.5;
Pred. No. 0.0
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Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                           any
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                                                                                                                                                                                                            of.
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Genew; HGNC:2188; COL12A1.

MIM; 120320; -.

GO; GO:0005595; C:collagen type XII; TAS.
GO; GO:0005501; P:skeletal development; TAS.
InterPro; IPRO03160; Collagen.
InterPro; IPRO03961; FN III.
InterPro; IPRO03961; FN III.
InterPro; IPRO03961; FN III.
InterPro; IPRO03961; WFA.
InterPro; IPRO03961; WFA.
Pfam; PF01391; Collagen; 4.
Pfam; PF01391; Collagen; 4.
Pfam; PF02210; TSP_N; 1.
Pfam; PF02210; TSP_N; 1.
Pfam; PF02010; TSP_N; 1.
Pfam; PF02010; TSP_N; 1.
PRINTS; PR00453; VWFA.
 Hydroxylation; 1
SIGNAL 1
CHAIN 25
DOMAIN 25
DOMAIN 333
DOMAIN 631
DOMAIN 722
DOMAIN 813
DOMAIN 904
DOMAIN 1086
DOMAIN 1199
DOMAIN 1199
DOMAIN 1384
DOMAIN 1565
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                                                                                                                                                                                                                                                                                       PROSITE; PS5085; FN3; 18.
PROSITE; PS50234; VMFA; 4.
PROSITE; PS50234; VMFA; 4.
Alternative splicing; Cell adhesion; Collagen;
Direct protein sequencing; Extracellular matrix; Glycoprotein;
Hydroxylation; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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each end (By similarity).
PTM: Prolines at the third position of
PTM: (G-X-Y) are hydroxylated in some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ittes requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: O-glycosylation of isoform Long; glycos; chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWPA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 short and long isoforms appear in amnion, chorion, skeletal muscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoform is found in lung, placenta, kidney and a squamous cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U73778; AAC51244.1;
U73779; AAD40483.1;
P18614; 1MHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q99715-2; Sequence=VSP_001149; SSUE SPECIFICITY: Found in collagen
 3063
112
316
422
316
616
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sunctation update)
01-JUN-2003 (TrEMBLrel. 24, Last sunctation update)
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-
length enriched library, clone:E330019B14 product:hypothetical vor
Willebrand factor type A domain containing protein, full insert
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W; 75FEA78FA8E48293
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Mus musculus

(Mouse)

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EP SEQUENCE FROM N.A.

(C STRAIN=C578L/61) TISSUE=Ovary;

(A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

(A Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

(A Pukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,

(A Hori F., Imotani K., Ishii Y., Ich M., Kagawa I., Kasukawa T.,

(A Hori F., Imotani K., Ishii Y., Ich M., Kagawa I., Kasukawa T.,

(A Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

(A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

(A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

(A Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,

(A Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,

(A Nishi K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

(A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

(A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

(A Sasaki D., Takahashi F., Takaku-Akshira S., Takeda Y., Tanaka T.,

(A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

(B MBL; AKO54356; BAC35749.1; -.

(B MBL; AKO54356; BAC35749.1; -.
PRINTS; PROUBLET; SM00327; "PES0234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/65; TISSUE=Ovary;

MRDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MRDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itch M., Aizawa K., Nagaoka T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Ovary;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh

Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cne RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meth.
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SEQUENCE FROM N.A.
STRAIN=(57BL/GJ; TISSUE=Ovary;
MEDLINE=99279253; pubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Ovary;
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Pfam, PF00092; VWA; 6.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                          MGD; MGI:2444259; E330026B02R1k.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN FANTOM Consortium;
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RIKEN Genome Explo
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602
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                                                      MSRDSVL----GPAHKLREENIRVHAIGVKEANQTQLREIAGEEKRVYYVHE-FDALRNI 601
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                                                                                                                                                             DIYLLIDGSGSTQPTDFHEMKTFLSEVVGMFNIAPHKVRVGAVQYADTWDLEFEISKYSN
RNOVVQEICAE
                                                                              BLHEDLFFYSERBANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGI
                                                                                                          KPDLGKAIENIROM--GGNTNTGAALNFTLKLLQRAKKE-----RGSKVPCHLVVLTNG
                           IHSILKKSCIE
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                           182
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                                                                                                                                                                                                                                          Length 1182;
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                                                                                                                                                                                                                 Gaps
                                                                                                           546
                                                                                                                                                               494
                                                                                 171
                                                                                                                                    111
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Search completed: June 13, Job time: 63.775 secs 2005, 20:03:15



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Minimum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-970-076-2_COPY_42_222
943
                                                                                               A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 13,
                                                                                                                                                                                                                                                                                                                                                      2105692 segs, 386760381 residues
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                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
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geneseqp1980s:*
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1044.623 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

						18 943							11 943	10 943		_	7 943				3 943	2 943	٣	Result No. Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	•	100.0	100.0		•		•	•	•	٠	•	100.0	100.0	Query Match
549	549	540	540	529	504	479	460	403	403	403	384	368	345	345	342	342	333	333	333	333	328	328	297	Length
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ADI00542	ADI00546	ADM64588	ADI00544	ADI00568	ADI00566	ADI00564	ADI00560	ADL77139	ABG63874	AAE01439	ADM64586	ABP54903	ADM64582	ADI00556	ADM64580	ADI00554	ADM64568	ADI00534	ABP54905	AAB01422	ADM64584	ADI00558	AAM38976	ID
					Adi00566 Human			Adl77139 Albumin	Human	Aae01439 Human gen	TANGO	Abp54903 Human ant			_	Adi00554 Human		Adi00534 Human		Aab01422 Human		8	Aam38976 Human	Description

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω u	32	31	30	29	28	27	20
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99.0	99.0	99.0	99.0	99.5	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	T00.0
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Abu54438	Abu54492	Abb90785	Abb90731	Ad177138	Abg63873	Aae01469	Adr48216	Adm64578	Adj70017	Adi00552	Abu54431	Abu54457	Abp54904	Abb90724	Abb90750	Adm64576	Adi00550	Adm64592	Adm64590
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US034263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001.
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23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-CCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344. Tang YT, Liu C, Asundi V, Chen R, Wang J, Wang Z, Wehrman T, Xu C, Zhou P, Goodrich R, Drmanac RT; WPI; 2001-442253/47. (HYSE-) HYSEQ INC. ма Хие Ŋ,ĸ Qian XB, Yang Y,

Ren F, I Zhang J,

Wang D; , Zhao QA;

Novel nucleic acids and polypeptides, useful as central nervous system injuries. for treating disorders **such** 

N-PSDB; AAI58132.

Example 4; SEQ ID NO 2121; 10078pp; English.

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                                                                                                             (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM4213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders. Note: The sequence data for this patent did not form
WPI; 2003-720708/68
                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003144193-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid pO615; mutein.
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                                                         Rottman JB,
                                                                                                                                                                                                                                                              20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                                     24-JUL-2002; 2002US-00201292
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                                                         O'keefe
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Pred. No. 1.7e-96;
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                                       (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                              antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vwF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax; inhalation anthrax; human; TANGO197; his tag; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 HiaTag fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-lik domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                                                                                             20-DEC-2001; 2001US-00038307
                                                                                                                                         20-DEC-2001; 2001US-00038307
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                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                          Human TANGO197-His tag fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                             ADM64584 standard; protein; 328
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Pred. No. 2e-96;
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Best Local Similarity 100
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising mature human TANGO197, thrombin cleavage site and his tag that can be used to treat exposure to or
                                                                                                                                                                           Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; j
                                                                                                                                                                                                                            TANGO, 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versue-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel diseases; septic shock; ulcerative collitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or amelilorating symptoms of anthrax comprises a von Willebrand factor A-liked domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                                                                                                                                                                                                                                                                                                                                                                                         AAB01422 standard; protein; 333 AA.
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   30-DEC-1998,
                                 23-DEC-1999;
                                                                                                                                                               prophylatic, therapeutic,
                                                                                                                                                                                                                                                                                                                                            20-OCT-2000
                                                                                                                               Homo sapiens
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DB; ADM64583.
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                                                                                                                                                                                                                                                                                                              TANGO 197.
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   98US-00223546
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Pred. No. 2e-96;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated
                                                                                                                                                                                                                                                                                                                        Human anthrax toxin receptor.
                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP54905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host disease, rheumatoid arthritis, psoriasis, inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid sequences encoding TANGO-128, and 239 polypeptides useful for the treatment of arthritis, psoriasis and autoimmune diseases.
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                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                 Anthrax; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP54905 standard; protein;
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Pred. No. 2e-96;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as a human anthrax toxin receptor (ATR) polypeptide of the basis of cidentity to a newly isolated human ATR (see ABP54903). The 2 polypeptides are identical between amino acids 1-317, but differ thereafter at the C-cerminus. The present polypeptide, encoded by IMAGE CLONE 4563020, has no previously known function, and there has been no prior indication that it is a complete or partial ATR. The invention provides ATR polypeptides and polymucleotides, vectors, host cells, and transgenic and knock-out polymucleotides, vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent that inhibits binding between anthrax toxin protective antigen (PA) and ATR at a level effective to reduce the severity of anthrax. Suitable agents include the present polypeptide or a PA-binding fragment of it, a PA-binding polypeptide at least 80% identical to these, a fusion protein, a muncleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 181; Conserv
  fusion; von Willebrand factor A-like domain; vWF; antibacterial;
                                               Human TANGO
                                                                                             22-APR-2004
                                                                                                                                                                                        ADI00534 standard; protein; 333 AA
                                                                                                                                             ADI00534;
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100.0%; Pred. No. 2e-96;
tive 0; Mismatches 0;
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Matches
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Best Local Similarity
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                03-JUN-2004
                                                                                                 ADM64568;
                                                                                                                                              ADM64568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 333 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-likedomain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
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  Willebrand factor
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                                                                                                                                           protein;
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100.0%; Pred. No. 2e-96;
tive 0; Mismatches
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protein TANGO197
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A-like

gene therapy;
factor A-like domain amino {
 sequence; anthrax; Bacillus

acid sequence; s anthracis; cutaneous anthrax;

A-like

domain

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RESULT 8
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Best Local Simi
Matches 181;
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           Human TANGO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 26; SEQ ID NO 2; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (VWP) amino acid sequence and an amino acid sequence heterologous
                               22-APR-2004
                                                 ADI00554;
                                                                    ADI00554 standard; protein;
                                                                                                                                                                                                                                                                                                                       Sequence 333
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                              (first entry)
           FLAG fusion
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          protein
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Pred. No. 2e-96;
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          plasmid p0613.
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         Human TANGO197-FLAG epitope
                              03-JUN-2004
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(OKEE/)
(OZKA/)
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)B; ADI00553.
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) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
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The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 FLAG fusion protein of the invention.
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ADM64580 standard; protein;
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Pred. No. 2.1e-96;
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fusion protein.

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RESULT 10
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Matches 181
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                   ADI00556;
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                                               ADI00556 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 342
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(OKEE/)
(OZKA/)
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DB; ADM64579.
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Pred. No. 2.1e-96;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                           <u>,</u>
                                                                                                                                                                                                                                                                                                           Score 943; DB 7;
Pred. No. 2.1e-96;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                               Length 345;
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Matches 181;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-likedomain (VWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 44; SEQ ID NO 24; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001US-00038307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TANGO197-His tag fusion
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                                                                                                                                                                                                                                                1 GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISFQLRWSFIVFSTRGTTLMKLTEDREQ
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OZKAYNAK E.
HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JB,
                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                  EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                                                                                                       IROGLEELOKVLPGGDTYMHEGFERASEQIYYENROGYRTASVIIALTDGELHEDLFFYS
                                                                                                                                         IRQGLEELQKVLPGGDTYMHEGFERASEQTYYENRQGYRTASVIIALTDGELHEDLFFYS
                                                                                                                                                                                                                   GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLKMSFIVFSTRGTTLMKLTEDREQ
  EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                          Score 943; DB 7;
Pred. No. 2.1e-96;
; Mismatches 0;
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                                                      Novel isolated polypeptide useful for identifying reduces effect of anthrax toxin on host cell, for
                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                         Region
                     Claim 1;
                                           human animal suffering from anthrax.
                                                                                         N-PSDB; ABV73881.
                                                                                                    WPI; 2002-713235/77.
                                                                                                                          Young JAT,
                                                                                                                                                                       05-DEC-2000; 2000US-0251481P
                                                                                                                                                                                             03-OCT-2001; 2001WO-US030941
                                                                                                                                                                                                                      13-JUN-2002.
                                                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anthrax; toxin;
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                                                                                                                                                                                                                                            WO200246228-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human anthrax toxin receptor
                                                                                                                                                (WISC ) WISCONSIN ALUMNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                    Page 29-30; 45pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                         Bradley KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor; human; antibacterial.
                                                                                                                                                                                                                                                                                                               motif with amino acid
                                                                                                                                                                                                                                                                                                                                                   motif with
                                                                                                                                                                                                                                                                                                                                                                                     motif with
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "forms metal ion-dependent adhesion
motif with amino acid residues 50, 54, 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                         motif with
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notif with amino acid residues 50, 52, 54 a
                                                                                                                                                                                                                                                                                                                                                                                  /note= "forms metal ion-dependent adhesion
notif with amino acid residues 50, 52, 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "forms metal ion-dependent adhesion
motif with amino acid residues 52, 54, 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         note= "forms metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "von Willebrand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "extracellular domain"
                                                                                                                                                                                                                                                                  "cytoplasmic
                                                                                                                                                                                                                                                                                          "putative transmembrane domain"
                                                                                                                                                 RES
                                                                                                                           Collier RJ,
                    English
                                                                                                                                                 FOUND
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id residues 50, 52, 54 a
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                                                      agent that prevents or treating human or non-
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and 150"
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and 150"
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and 150"
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present sequence is the protein sequence of a human surface- bound

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RESULT 13
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AC ADM64
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XX ANTIL
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XX VWF a SYNIT
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YX US20(
YX ITANGO
OS SYNIT
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Best Local Similarity
  WPI; 2003-829643/77
N-PSDB; ADM64585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vwr amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax; inhalation_anthrax; human; TANGO197; immunoglobulin G; IgG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anthrax toxin receptor (ATR), as predicted from an isolated cDN Anthrax toxin protective antigen (PA) binds to the ATR at a vor Willebrand factor A domain located in the extracellular domain
                                                                                   Rottman JB, O'keefe
                                                                                                                                                                         (OKEE/)
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                                                                                                                                      ) ROTIMAN J B.
) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
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                                                                                      Ozkaynak E,
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                                                                                                                                                                                                                                                                      Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; foetal abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; chemotaxis; food additive; gene therapy; binding partner identification.
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                                                                                                                                                                                          Homo sapiens
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                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
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L235A and G237A.
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                                                            /label=_Signal_peptide
                                                                                                                        Location/Qualifiers
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Pred. No. 2.5e-96;
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Protein

"Mature human secreted

protein"

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Matches 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999; 99US-0163581P
30-JUN-2000; 2000US-0215133P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 485-486; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions
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                                             EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
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                                                                                                                                                                                                                                                                                                                                                                            Sequence
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/backfIles1.pep:*
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US-09-193-043-37
US-09-193-043-37
US-08-485-618-55
US-08-945-652-55
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US-09-193-043-55
US-09-193-043-50
US-09-193-043-56
US-08-485-618-46
US-08-688-3077-46
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/08286889 Patent No. 5470953
   Matches
              Query Match
Best Local
                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION = 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                         TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: 'Toole, Gerstein, Murray & ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MERAL INFORMATION W. MICH
APPLICANT: Gallatin, W. MICH
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5470953el Human
                                                            MOLECULE TYPE: protein
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  Local Similarity
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TYPE: amino acid
TOPOLOGY: linear
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CITY: Chicago
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7: United States
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US-09-193-043-53

US-09-188-307A-53

US-09-350-259-53

US-09-795-872-5

PCT-US95-04439-1

US-08-476-062A-43

PCT-US95-01314-43

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  38; Mismatches
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US-08-286-889-3

US-08-485-618-3

US-08-362-652-3

US-08-605-672-3
Score 141.5; DB 1;
Pred. No. 4.2e-07;
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                                                                                 Matches
                                                                                                                                                                 MOLECULE TYPE: protein -08-485-618-37
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PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/362,6
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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LENGTH: 1151 amino aci
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SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Chicago
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                                    3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                             h 15.0%; Score 141.5; DB 1; Length 1151;
Similarity 27.7%; Pred. No. 4.2e-07;
53; Conservative 38; Mismatches 75; Indels 25;
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Best Local Similarity
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Patent No. 5766850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY, AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/286,889 FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 166
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                                                                              57 DREQIRQGLEELOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
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                                          DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELPHSKNGSRKSAKKILLVITDGQKYRD
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
                                                                                                                                                                                                     15.0%; Score 141.5; DB 1; 27.7%; Pred. No. 4.2e-07; ative 38; Mismatches 75;
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RESULT 4
US-08-605-672-37
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US-08-605-672-37
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                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                         Query Match
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APPLICATION UNMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,559
REFERENCE/DOCKET NUMBER: 27866/32684
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APPLICANT: Gallat
APPLICANT: Van de
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 233 SC
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 60606-6402
                                                                                                                                                                                                                                                     Local
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                                    116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 166
                                                                           202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
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                                                                                                                                                     142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
                                                                                                                                                                                                                                    53,
                                                                                                                                                                                                                                                       Similarity
PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                                DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
                                                                                                                                                                                           DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                15.0%; Score 141.5; DB 2; 27.7%; Pred. No. 4.2e-07; tive 38; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
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                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                    Indels
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US-08-482-293A-37
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                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                Query Match
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3268.
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 200
STREET: Chicago
CITY: Chicago
Illinois
Thnited
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                         116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 166
                                                                                                                                                                                             142 DIAFLIDGSGSINORDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
                                                                                                                                                     57 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                  3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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5831029
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                                      PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                                DPOSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
LQGIIHSILKK 177
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                           15.0%; Score 141.5; DB 2
27.7%; Pred. No. 4.2e-07;
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US-08-943-363-37
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                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein -08-943-363-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/286,889
PILING DATE: 5-AUG-1994
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
313
                                   167 LOGIIHSILKK 177
                                                                             257
                                                                                                            116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNB-TQLARI-----ADSKDHVFPVNDGFQA 166
                                                                                                                                                          202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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LRSIQRQLQEK 323
                                                                               PLEYSDVI PAADKA ---
                                                                                                                                                                                               DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                             -GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
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; ORGANISM: Rattus rattus
US-09-193-043-37
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US-09-193-043-37
                                        CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION UNMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR TILING DATE: 1996-02-22
PRIOR PPLICATION NUMBER: 08/173,497
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR APPLICATION NUMBER: 08/286,869
PRIOR APPLICATION NUMBER: 08/266,869
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CURRENT APPLICATION NUMBER: US/09/193,043

CURRENT FILING DATE: 1998-11-16

EARLIER APPLICATION NUMBER: 08/173,497

EARLIER APPLICATION NUMBER: 08/286,889

EARLIER FILING DATE: 1994-08-05

EARLIER APPLICATION NUMBER: 08/286,689

EARLIER APPLICATION NUMBER: 08/362,652

EARLIER APPLICATION NUMBER: 08/363,363

EARLIER APPLICATION NUMBER: 08/943,363

EARLIER APPLICATION NUMBER: 08/943,363

EARLIER FILING DATE: 1994-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn SEQ ID NO 37
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                                                                                                                                                                                                                                                                                                 APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, Michae
APPLICANT: Van der Vieren,
TITLE OF INVENTION: No. 629
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gallatin, APPLICANT: Van der
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APPLICATION I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
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NUMBER: 08/943,363
                       1994-12-21
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27.7%;
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Pred. No. 4.2e-07;
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256

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GENERAL INFORMATION:

APPLICANT: Gallatin, Michael W.

APPLICANT: Gallatin, Michael W.

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 66209161 Human 2

FILE REFERENCE: 27866/35004

CURRENT APPLICATION NUMBER: US/09/350,259

CURRENT FILING DATE: 1999-07-08

EARLIER APPLICATION NUMBER: 09/193,043

EARLIER APPLICATION NUMBER: 09/193,497

EARLIER APPLICATION NUMBER: 08/173,497

EARLIER FILING DATE: 1993-12-23

EARLIER FILING DATE: 1993-12-23

EARLIER FILING DATE: 1994-12-21

EARLIER APPLICATION NUMBER: 08/362,652

EARLIER APPLICATION NUMBER: 08/362,652

EARLIER APPLICATION NUMBER: 08/943,363

EARLIER FILING DATE: 1997-10-03

NUMBER: DESQ ID NOS: 114
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US-09-350-259-37
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SOFTWARE: PatentIn
SEQ ID NO 37
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Patent No. 6620915
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SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
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LOCATION: 464
OTHER INFORMATION: Xaa = a
NAME/KEY: misc_feature
LOCATION: 486
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TYPE: PRT
ORGANISM: Rattue rattue
PEATURE:
PEATURE:
NAME/KEY: misc_feature
LOCATION: 361
OTHER INFORMATION: Xaa = a
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LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
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LOCATION: 1117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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Best Local Similarity 27.7%; Pred. No. 4.2e-07
Matches 53; Conservative 38; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 28,659
REFERENCE/DOCKET NUMBER: 27866/3279
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 233 SOUTH
                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFFVNDGFQA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
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                                                                  1161 amino acids
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                            312-474-0448
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RESULT 11
US-08-362-652-55
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                                                               TOPOLOGY: 11;

MOLECULE TYPE:
US-08-362-652-55
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 Best Loc
Matches
               Query Match
Best Local Similarity
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                                                                                                                                                            TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: US 08/
PILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
PILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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CITY: Chicago
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                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                             amino
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                               1161 amino acids
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                 linear
                                                                                                                                                                                                                 312-474-6300
                                                                                                                   acid
                                                                              protein
15.0%; Score 141.5; DB 1 27.7%; Pred. No. 4.2e-07; tive 38; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                               US 08/173,497
                                                                                                                                                                                                                                                                                                                                 US 08/286,889
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                              DB 1;
                              Length 1161;
 Indels
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25;
Gaps
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                              Matches
                                                               Query Match
                                                                                                                               TYPE: ami
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Sequence 55, Apprased No. 5817515
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GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/286,889

PRIOR APPLICATION NUMBER: US 08/286,889

PILING DATE: 5-AUG-1994

PRIOR APPLICATION NUMBER: US 08/362,652

PILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                    TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 1161 amino aci
                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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APPLICATION NUMBER: US 08/173,497
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTPTEFKNIL
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3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Illinois
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                          1161 amino acids
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                                            Conservative
                                                                                                                                                     protein
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                                     Score 141.5; DB 2;
Pred. No. 4.2e-07;
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                                            Indels
                                                                                   Length 1161;
                                            25;
                                            Gaps
    56
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                                                            Matches
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                                                                                          Query Match
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                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 21-DEC-1994
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ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marchall, O'Toole, Gill Sear Tower
                                                                                                                                       TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                      TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                           Local Similarity
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                           3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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DIAPLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
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                                                                                                                                                                                       1161 amino acide
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                                                            Conservative
                                                                                                                                                                                                                                                                     312-474-6300
                                                                                                                                         protein
                                                                         15.0%;
27.7%;
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                                                                                                                                                                                                                                                                                                        38,659
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                                                            38;
                                                         Score 141.5; DB 2;
Pred. No. 4.2e-07;
88; Mismatches 75;
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                                                            Indels
                                                                                        Length 1161;
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                                                         Gaps
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                                                                       Matches
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                                                                                                      Query Match
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC comm
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human
                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                       Local Similarity
                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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 152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
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                                   DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US 08/286,889
5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1994
                                                                      15.0%; Score 141.5; DB 27.7%; Pred. No. 4.2e-07 ative 38; Mismatches 7
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                                                                                                        DB 2;
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                                                                                                        Length 1161;
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57 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115

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US-09-193-043-55

Sequence 55, Application US/09193043

Patent No. 6251395

GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395e1 Human 2
FILE REFERENCE: 27866/35004

CURRENT APPLICATION NUMBER: US/09/193,043

CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/366,889
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 55
LENGTH: 1161
TYPE: PRT
ORGANISM: Rattus rattus
US-09-193-043-55
Search completed: June 13, 2005, 20:05:10 Job time : 18.6748 secs
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                                                                           323
                                                                                                            167 LOGIIHSILKK 177
                                                                                                                                                267 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
                                                                                                                                                                                   116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFYNDGFQA 166
                                                                                                                                                                                                                         212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                  Score
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seq length: 2000000000
      Query
Match
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-038-307-26

US-10-201-292-26

US-09-796-753-12

US-10-038-307-2

US-10-038-307-2

US-10-038-307-22

US-10-038-307-24

US-10-038-307-24

US-10-038-307-24

US-10-038-307-24

US-10-201-292-24

US-09-833-245-621

US-10-201-292-28
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                  Sequence 26, AppI
Sequence 12, AppI
Sequence 2, AppIi
Sequence 2, AppIi
Sequence 22, AppII
Sequence 22, AppII
Sequence 22, AppII
Sequence 24, AppII
Sequence 24, AppII
Sequence 24, AppII
Sequence 24, AppII
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10	15	14	14	14	10	13	14	14	14	14	14	14	14	14	14	16	16	10	10	11	16	16	16	14	14	14	10	10	14	14	14	14	14
96-753-	-10-104-047-2	-10-368-087-1	-10-201-292-	0-038-307-	-09-796-753-5	-10-047-542-	-10-201-292-1	-10-201-292-1	-10-201-292-1	-10-038-307-1	-10-038-307-1	-10-038-307-	-10-201-292-1	-10-038-307-1	-10-201-292-	-10-474-794-3	-794-1	-09-918-715-3	-09-918-715-1	-09-833-245-6	0-474-79	-10-474-794-1	-10-408-765A-	01-822-1	-10-201-292-2	-10-038-307-	18-715-2	-09-918-715-1	-10-201-292-1	-10-038-307-	92-3	-10-201-292-3	92-
equence 54	e 2639	equence 16	equence 6,	equence 6,	equence 52	equence 99	equence 16	equence 14	equence 10	equence 16	equence 14	e 10	equence 12,	equence 12,	30,	301,	194,	301,	194,	620,	w	≥ 187,	1823	199,	20,	20,	232	187,	18,	18,	36,	quence 34,	Sequence 32, Appl

## ALIGNMENTS

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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

ITTLE OF INVENTION: Tango 197 and Tango 216 Compositions and Metler

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 328

TYPE: PAT

ORGANISM: Homo Bapiens

US-10-038-307-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-038-307-26
US-10-038-307-26
; Sequence 26, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                    Matches
                                             102
121 EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI 180
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                                                                                  IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS 120
                                                                                                                                  GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ 101
                                           IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR PELLING DATE: 1998-10-30
PRIOR PELLING DATE: 1998-12-30
PRIOR PELLING DATE: 1998-12-30
PRIOR PELLING DATE: 1998-12-30
PRIOR PELLING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILLING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR PELLING DATE: 1999-02-26
PRIOR PELLING DATE: 1999-03-03
PRIOR PELLING DATE: 1999-03-03
PRIOR PELLING DATE: 1999-03-03
PRIOR PELLING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
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US-09-796-753-12
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US-10-201-292-26
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US-10-201-292-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 328
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 943; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-90; Matches 181; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 IRQGLEELQKYLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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RESULT 4 US-10-038-307-2

Sequence 2, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN

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; ORGANISM: Homo sapiens
US-09-796-753-12
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SEQ ID NO 12
LENGTH: 333
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2000-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR APPLICATION NUMBER: 09/4:
DR FILING DATE: 1999-12-23
DR APPLICATION NUMBER: 09/4:
DR APPLICATION NUMBER: 09/4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R FILING DATE: 1999-05
R APPLICATION NUMBER:
R FILING DATE: 1999-06
R APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/5
FILING DATE: 2000-03-01
APPLICATION NUMBER: 09/5
FILING DATE: 2000-05-14
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PTT.TNG DATE: 2000-06-19
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APPLICATION NUMBER: 09/
FILING DATE: 2000-02-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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FILING DATE: 2000-06-22
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FILING DATE: 1999-07-30
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                                                                               121 EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSCI 180
                           181 ¥ 181
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                                                                                                                                           IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS 120
M.
                                                            EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                                                                                                                         IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
222
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100.0%; Pred. No. 1.6e-90;
rative 0; Mismatches 0;
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-201-292-2
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j ORGANISM: Homo sapiens
US-10-038-307-2
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APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT PILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10201292 Publication No. US20030144193A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Query Match 100.0%; Score 943; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-90; Matches 181; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100
Best Local Similarity 100
Matches 181; Conservative
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                                                                                   102 IROGLEELOKVLPGGDTYMHEGFERASEQIYYENROGYRTASVIIALTDGELHEDLFFYS
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                                                                                                                            61 IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS 120
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EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                           EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSCI 180
                                                                                                                                                                       GPDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
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100.0%; Pred. No. 1.6e-90;
***ve 0: Mismatches 0;
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US-10-201-292-22

; Sequence 22, Application US/10201292

; Publication No. US20030144193A1
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; ORGANISM: Homo sapiens
US-10-038-307-22
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                                                                                                   ) ORGANISM: Homo sapiens
US-10-201-292-22
                                                                                                                                                         APPLICANT: James B. ROTTMAN
APPLICANT: Theres L. O'KEEFE
APPLICANT: Theres L. O'KEEFE
APPLICANT: Theres L. O'KEEFE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE. DET
Query Match
Best Local Similarity
Matches 181; Conserv
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SEQ ID NO 22
LENGTH: 342
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT ENFLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                TYPE: PRT
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       100.0%; silarity 100.0%; F
Conservative 0;
       Score 943; DB 14;
Pred. No. 1.7e-90;
; Mismatches 0;
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           Indels
                                                      Length 342;
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1 GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ 60

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US-10-201-292-24

; Sequence 24, Application US/10201292

; Publication No. US20030144193A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-24
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US-10-038-307-24
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GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions
FILE REFERENCE: 7853-253-999
FILE REPERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
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Publication No. US20030134786A1
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CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PALENTIN Ver. 2.1
; SEQ ID NO 621
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; ORGANISM: Homo sapiens
US-10-201-292-24
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LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 621, Application No. US200 GENERAL INFORMATION:
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Best Local Similarity
Matches 181; Conserv
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PF546PCT
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 403
                               181
                                                                162 EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                                                                                     121 EREANRSRDIGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                                                                                                                                   102 IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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222 E
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                                                                                                                                                                                                                                                                     181; Conservative
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                                                                                                                                                        IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS 120
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                                 181
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                                                                                                                                                                                                                                                                   100.0%; Score 943; DB 11; 100.0%; Pred. No. 2.1e-90; O. Mismatches 0;
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                                                                                                                                                                                                                                                                                                    Length 403;
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                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-32
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-28
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Engin OZKAYNAK

APPLICANT: LOST INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT PILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOPTWARE: FastSEQ for Windows Version 4.0

SOPTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REPERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION SERVICES 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 28
                                                                                                                                                                   Query Match 100.0%; Score 943; DB 14; Best Local Similarity 100.0%; Pred. No. 2.7e-90; Matches 181; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/10201292 Publication No. US20030144193A1
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Best Local Similarity 100.
Matches 181; Conservative
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Publication No. US20030144193A1
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                      61 IRQGLEELQKVLPGGDTYMHEGFERASEQTYYENRQGYRTASVITALTDGELHEDLFFYS
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                                                                                                          1 GPDLYFILDXSGSVLHHWNBIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
                                                                                 GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
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IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNA
APPLICANT: Engin OZKAYNA
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 504
TYPE: PRT
GOGANISM: Homo sapiens
US-10-201-292-34
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US-10-201-292-36
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; ORGANISM: Homo sapiens
US-10-201-292-36
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US-10-201-292-34
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                                     NUMBER OF SEQ ID NOS: 36
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 529
TYPE: PRT
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                                                                                                                                    APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
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Local Similarity 100.0%;
nes 181; Conservative 0
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Pred. No. 2.9e-90;
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RESULT 15
US-10-038-307-18
WS-10-038-307-18
Sequence 18, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: JUGith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
UNMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
Search completed: June 13, 2005, 20:36:52 Job time : 59.0354 secs
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-18
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RESULT 2
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cell surface glycoprotein CD11b precursor [validated] - human
cell surface glycoprotein CD11b precursor [validated] - human
cell surface glycoprotein CD11b precursor [validated] - human
cell surface glycoprotein cD11b precursor type 3 alpha chain; leukocyte adhesion
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Ju1-2004

protein

Mac

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QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHED	Score 136; DB 2; Pred. No. 0.00074; ; Mismatches 79; ;YYFVEQLAHKF-ISP-QLR  ;   ;   ;   RSFISNFAGIMPLSPDDVR	NCBI backbone (NCBIN:123776, ) factor type A repeat homology fayer repeat homology <thr1 1="" <thr2="" <thr4="" <thr5="" <thr5<="" homology="" repeat="" td="" type=""><td>in, M:, Weber, G. 174, 1993 ria maxima antigen hc 93149203; PMID:842661</td><td>ALLIGNMENTS ision 18-Nov-1994 #te</td><td>AB1079 ITECAP B91018 B9162 B085862 VZEBPT VZEBPT ALIGNMENTS</td><td>\$04531 \$40970 \$470970 \$17797 \$150889 \$132949 \$462350 \$62285 \$83262 \$84811</td></thr1>	in, M:, Weber, G. 174, 1993 ria maxima antigen hc 93149203; PMID:842661	ALLIGNMENTS ision 18-Nov-1994 #te	AB1079 ITECAP B91018 B9162 B085862 VZEBPT VZEBPT ALIGNMENTS	\$04531 \$40970 \$470970 \$17797 \$150889 \$132949 \$462350 \$62285 \$83262 \$84811
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A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-499,501-1153 <FLE>
A;Cross references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID
A;Note: the last three bases of intron 13, CAG, are included in (A;Note: sequence extracted from NCBI backbone (NCBLP:121963)
A;Note: sequence extracted from NCBI backbone (NCBLP:121963)
A;Note: sequence extracted from NCBI backbone (NCBLP:121963)
A;Pietrce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M Biochim. Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mol A;Reference number: A90664; MUID:87076671; PMID:3539202
A;Accession: A26091
A;Molecule type: protein
A;Residues: 17-31 <PIE>
A;Residues: 17-31 <PIE>
A;Reparimental source: granulocytes
R;Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
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A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218
A;Accession: A32218
A;Molecule type: mRNA
A;Residues: 9-1153 <HIC>
A;Residues: 9-1153 <HIC>
A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A;Note: part of this sequence was confirmed by protein sequencing R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
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A;Title: Molecular cloning of the alpha-subunit of human and A;Reference number: A94193; MUID:88190151; PMID:2833753
A;Accession: A30892
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Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A;Title: The promoter of the CD11b gene directs myeloid-specific and developmentally A;Reference number: A41600; MUID:92073318; PMID:1683702
A;Accession: A41600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Structural analysis of the CD11b gene and phylogenetic analysis n during evolution.
A;Reference number: A46526; MUID:93123748; PMID:8419480
A;Accession: A46526
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A;Note: part of this sequence was confirmed by protein sequencing
R;Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
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A; Residues: 1-11
A; Cross-reference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A31108; MUID:88315033; PMID:2457584 A;Accession: A31108
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A; Residues: 917-1042 < AR2>
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A; Residues: 1-9 <SHE>
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A; Residues: 1-499,501-965, 'P', 967-1153 < ARN >
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N;Alternate names: fibrochimerin
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S22524; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obara
J. Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule winous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule winous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A;Reference number: A40020; MUID:92011862; PMID:1918137
A;Accession: A40020
A;Molecule type: manA
A;Residues: 1-3124 <YAM>
A;Residues: 1-3124 <YAM>
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A;Cross-references: GB:M84477; NII
A;Cross-references: GB:M84477; NII
C;Comment: A common beta chain (CI
C;Genetics:
A;Gene: GDB:ITGAM; CR3A
A;Cross-references: GDB:120599; ON
A;Cross-references: GDB:12-16p11.2
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F;1109-1134/Domain: intracellular #status predicted <INT>
F;86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; magn
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F;17-1108/Domain: extracellular #status predicted <EXT>
F;18-318/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g2
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                                                                                    A;Molecule type: protein
A;Residues: 2772-2792;2846-2873 <GOR2>
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    Natl. Acad.
M.K.; Gerecke, D.R.; Olsen, B.R.
l. Acad. Sci. U.S.A. 84, 6040-6044,
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Pred. No. 0.0026;
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extracellular

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A;Reference number: A28037; NULLICITION AND A;Reference number: A28037
A;Accession: A28037
A;Molecule type: mRNA
A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
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A;Molecule type: mRNA
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
C;Genetics:
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A,Title: Type XII collagen is expressed in embryonic chick tendons. A,Reference number: $22254; MUID:88087065; PMID:3121603
A,Accession: $22254
A,Molecule type: protein
A,Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
R,Trueb, J.; Trueb, B.
R,Trueb, J.; Trueb, B.
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A;Title: A major oligomeric fibroblast proteoglycan identified A;Reference number: S23814; MUID:92362621; PMID:1323460
A;Accession: S23814
A;Accession: S23814
A;Molecule type: protein
A;Molecule type: protein
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A;Molecule 'X',1333,'O',1335-1347;1914-1928;2504,'X',2506,'X',
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A,Title: The two splice variants of collagen XII share a
A,Reference number: S28811; MUID:93042014; PMID:1420368
A,Accession: S28811
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                                                                                                                                                        F;2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>F;2946-3048/Domain: collagenous COL1 #status predicted <COL1>F;2946-3048/Domain: non-collagenous NC1 #status predicted <COL1>F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>F;32,1006;1032;1044,1512;1767,2210,2273,2532,2683/Binding site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;2325-2490/Domain:
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1366-1647/Domain: fibronectin type III repeat homology FN3I>
1365-138/Domain: fibronectin type III repeat homology FN3I>
1365-138/Domain: fibronectin type III repeat homology FN3I>
1365-138/Domain: fibronectin type III repeat homology FN3I>
1375-138/Domain: fibronectin type III repeat homology FN3I>
137-2019/Domain: fibronectin type III repeat homology FN3I>
137-2019/Domain: fibronectin type III repeat homology FN3I>
137-2019/Domain: fibronectin type III repeat homology FN3I>
1319-2199/Domain: fibronectin type III repeat homology FN3I>
1319-3199/Domain: fibronectin type III repeat homology FN3I>
1319-31
                                                                                                                                                                                                                                                                                              ,2438-2440/Region: cell adhesion #status predicted
,2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted
,2751-2902/Domain: collagenous COL2 #status predicted <COL2>
,2899-2901/Region: cell attachment (R-G-D) motif
                  Best Local Similarity
                                                    Query Match
                                                                                                                          006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline
                  13.6%;
26.3%;
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                  Score 128; DB 2;
Pred. No. 0.021;
                                                    Length 3124
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N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain C;Species: Homo sapiens (man) C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004 C;Accession: A36584; A35543; S00864 R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A. J. Biol. Chem. 265, 12750-12751, 1990
                                                                                                                                                                                                                                                                           RESULT
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A;Cross-references: UNITADA NCBI backbone (NCBIN:///34, NCF A;Note: sequence extracted from NCBI backbone (NCBIN:///34, NCF A;Note: sequence extracted from NCBI backbone (NCBIN:///34, NCF A;Note: sequence extracted from logy < THR1 > F;48-218[)Oomain: von Willebrand factor type 1 repeat homology < THR2 > F;309-371/)Oomain: thrombospondin type 1 repeat homology < THR3 F;432-432/Domain: thrombospondin type 1 repeat homology < THR4 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR5 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homology < THR6 > F;494-556/Domain: thrombospondin type 1 repeat homo
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A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064; PMID:1775171
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A; Residues: 1-712 < TOM>
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216 SNWSNVTQQVNGIIKAAC 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDRB
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                                                                          DGFQALQGIIHSILKKSC
                                                                                                                                                                                                                                  IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP--VN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKAQALGALQNVQ--YRGGNTRTGKALTFIKEKVLTWESGMRRGVPKVLVVVTDGRSQDE
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Pred. No. 0.0
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leukocyte adhesion recept

human

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C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on C;Genetics:
A;Gene: GDB:ITGAX; CD11C
A;Gene: GDB:ITGAX; CD11C
A;Gene: GDB:ITGAX; CD11C
C;Genetics:
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat he C;Superfamily: cell adhesion; glycoprotein; heterodimer; magnesium; tandem repe; p;1-19/Domain: signal sequence #status predicted <SIG>F;10-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>F;10-1107/Domain: von Willebrand factor type A repeat he crown fills form intracellular #status predicted <TMM>F;1108-1133/Domain: intracellular #status predicted <TMM>F;1134-1163/Domain: intracellular #status predicted <TMM>F;1134-1163/Domain: intracellular #status predicted <TMM>F;1134-1163/Domain: intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1134-1163/Domain: black intracellular #status predicted <TMM>F;1145/Domain: bla
                                                                                                                                                    leukocyte surface glycoprotein Mac-1 alpha chain precursor - N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_chan C;Accession: S00551; I59078 R;Pytela, R. R. Pytela, R. Pytela, R.
A; Molecule
                                A;Title: Amino acid sequence
A;Reference number: S00551;
A;Accession: S00551
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A;Residues: 1-755,'L','757-1163 <CO3>
A;Residues: 1-755,'L','757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
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J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit,
A;Reference number: A35543; MUID:90153906; PMID:2303426
A;Accession: A35543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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A; Residues: 1-834 < CO2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
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Cross-references: UNIPROT:P20702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 NPLSLLASVHQLQ
    type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND-----IASKPSQEHIFKVED-
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                                                                    of the murine MUID:88312584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD
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K.; Larson, R.S.; S
                                                                        Mac-1 alpha
PMID:3044779
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                                                                                                                chain
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: $42368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T20G5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #tC;Accession: S42373 R;Smith, A.
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A; Cross-references: EMBL
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A; Residues: 11-44 < RES>
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Best Local
                                                                                                                                                                                       Matches
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                                                                                                                                     3 DLYFILDKSGSVLHH--WNEIYYFVEQLAHKFI--SPQLRMSFIVFSTRGTTLMKLTE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED--
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                                                                                                                                                                                                                Similarity
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                                          DREQIRQGLEELQKVLPG----GDTYMH---
                                                                                         DLVFLIDGSGSIGSYVFKNEVLRFVREFVELFEIGRSKTRVGLIQYSDQIRHEFDLDQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V-DNFEALNTIQUOLQEK
DRDSLLKGISETQ-YLTGLTRTGAAIQHMVQEGF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT
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                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                             12.3%;
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                                                                                                                                                                                                             Score 116;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-Nov-1995 #text_change 09-May-2004
                                          EGFERASEQIYYENROGYR----TASVI 104
                                                                                                                                                                                                                                                                                                      A repeat homology <VWA1>
homology <2F1>
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                                                                                                                                                                                                                                 Length 3051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                     952/2; 1041/1; 1146/1;
                                                                                                                                                                                       Gaps
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A Cross-references: UNIPROT: P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1;
A. Stol. Chem. 265, 1904-19046, 1990

J. Biol. Chem. 265, 1904-19046, 1990

A. Witle Markine complement C2 and factor B genomic and cDNA cloning reveals different me AlReference number: A36593; MUID:9103430; PMID:2229060

A. A. Cross-references: EMBL:M57891; NID:g192436; PIDN:AAA63294.1; PID:g192437

A. Walscule type: makk

A. Residues: 1-760 <a href="https://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.
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A;Accession: A38876
A;Molecule type: DNA
A;Residues: 1-760 <182>
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Best Local S
Matches 52
                                                                                                                                                                                                                    261 NLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILSERS
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                                                                                                 60 QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE------NRQGYRTAS----
                                                                                                                                                                                                                                                                                                                      3 DLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTEDRE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
Q-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAWKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%; Score 114.5; DB 1;
24.3%; Pred. No. 0.056;
41. Mismatches 72;
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     374
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F:236-317/Domain: fibronectin type III repeat homology <FNJA>
F;326-409/Domain: fibronectin type III repeat homology <FNJA>
F;418-498/Domain: fibronectin type III repeat homology <FNJB>
F;507-591/Domain: fibronectin type III repeat homology <FNJD>
F;507-591/Domain: fibronectin type III repeat homology <FNJD>
F;625-707/Domain: fibronectin type III repeat homology <FNJB>
F;716-798/Domain: fibronectin type III repeat homology <FNJB>
F;806-893/Domain: fibronectin type III repeat homology <FNJG>
F;806-893/Domain: fibronectin type III repeat homology <FNJG>
F;924-1089/Domain: non-collagenous NC4 #Status predicted <NC4>
F;1111-1353/Domain: non-collagenous NC2 #Status predicted <NC2>
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A;Cross-references: UNIPROT:P32018
A;Experimental source: embryo skin
A;Experimental source: embryo skin
A;Experimental source: sequence inconsistent with the nucleotide translation
A;Nore: sequence inconsistent with backbone (NCBIN:133364, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1551-1570;1593-1599;1639-1667 < GOR2>
A; Residues: 1551-1570;1593-1599;1639-1667 < GOR2>
C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime: F;40-204/Domain: von Willebrand factor type A repeat homology < VWA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne,
Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Reference number: S17035; MUID:92037585; PMID:1935930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, March 1992
A;Reference number: S30085
A;Accession: S30085
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A;Accession: A45974
A;Status: preliminary
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C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A45974, S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Canc J. Biol. Chem. 268, 12177-12184, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1472-1659 <GOR1>
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Eur. J. Biochem. 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1472-1660 < APT >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA; protein
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                                                                                                                                                    F;1554-1659/Domain: triple helical domain COL1 #status predicted
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                                        Query Match
Best Local :
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                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKELNE 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LGSKKDGERHAFILQDA-KALQQIFEHMLDVS
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                                12.0%; Score 113; DB 2; 26.1%; Pred. No. 0.2;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.; Gennari, M.; Dublet, B.; Cancedda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178
                                                                        Length 1747;
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                                                                                                                                                        <C0L1>
Gaps
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3 DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 56

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R;Waelchll, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Blochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: 331211; MUID:93185668; PMID:8444186
A;Accession: S31212
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1857 <MAES
A;Cross-references: EMBL:X70792; NID:9288874; PIDN:CAA50063.1; PID:9288875
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CO114A1

C;Keyworde: alternative splicing; coiled coil; extracellular matrix; glycoprotein;

F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;352-433/Domain: fibronectin type III repeat homology <FN3D>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;423-707/Domain: fibronectin type III repeat homology <FN3B>
F;533-614/Domain: fibronectin type III repeat homology <FN3B>
F;741-823/Domain: fibronectin type III repeat homology <FN3G>
F;741-823/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3H>
F;832-1019/Domain: fibronectin type III repeat homology <FN3H-
F;832-1019/Domain: fibronectin type III repeat homolo
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C;Date: 11-Ma.
C;Accession: C;R;Waelchli, C
Eur. J. Bloch
collagen alpha 1(XIV) chain precursor, C;Species: Gallus gallus (chicken)
                                                                             S78476
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C;Species: Gallus gallus (chicken)
C;Datc: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 1101
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                                                                                                                                                                                                                                                                                           HSILKKSC 179
                                                                                                                                                                                                                                                                                                                                                                DV-----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE
                                                                                                                                                                                                                                                                                                                                                                                                                        DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
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                                            chicken
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C;Accession:
R;Trueb, B.
                             A;Cross-references: UNIPROT:Q91145; EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g63264
F;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                              A,Title: Monoclonal antibody MT2 identifies the urodele alpha A,Reference number: I51027; MUID:95246925; PMID:7729585 A,Accession: I51027
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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I51027
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A; Residues: 1-929 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
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Best Local :
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Biol. 168, 503-513, 1995
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F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3C>
F;623-707/Domain: fibronectin type III repeat homology <FN3B>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;341-823/Domain: fibronectin type III repeat homology <FN3F>
F;831-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
F;921-009/Domain: fibronectin type III repeat homology <FN3G>
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F;29-188/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FW3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
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A;Residues: 1-416;1460-1811,1843-1888
A;Cross-references: EMBL:X70793
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A;Residues: 1-1888 <TRU>
A;Cross-references: UNIPROT:p32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1; PID:g28887
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
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A;Reference number: S31211; MUID:93185668; PMID:8444186
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A;Reference number: S78476
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Accession: S78476; S31211
1213 DELITFVC 1220
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                                                                                     HSILKKSC 179
                                                                                                                                                                          DV-----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE 1212
                                                                                                                                                                                                                                                      DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII
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chain

of type XII collage

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C/Species: Homo sapiens (man)
C/Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text change 09-Jul-2004
C/Accession: A54849, PH0844; $16316; I56328; A30296; I84686
R/Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of t.
A;Reference number: A54849; MUID:94327588; PMID:8051117
                                                                                                A;Experimental source: keratinocyte
R;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright,
J. Invest. Dermatol. 99, 691-696, 1992
A;Fitle: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion
A;Reference number: I56328; MUID:93107742; PMID:1469284
A;Accession: I56328 MUID:93107742; PMID:1469284
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Hesidues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A;Geldues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A;Geldues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A;Geltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson,
J. Biol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV colla
A;Accession: A30296; MUID:89139437; PMID:2537292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Molecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 'EFR',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C'A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699 A;Experimental source: keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A;Title: Molecular cloning and characterization of type A;Reference number: PH0844; MUID:92231902; PMID:1567409 A;Accession: PH0844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-2944 < CHR>
A; Cross-references: UNIPROT: Q02388; GB: L02870; NID: g987124; PIDN: AAA75438.1; PID: g98712
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,Residues: 815-892,'E',894-1439 <PAR>
,Cross-references: GB:M65158, GB:S49017, NID:g180914, PIDN:AAA96439.1, PID:g180915
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Best Local Similarity
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F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BP F;337,786,1109/Binding site: carbohydrate (Asn) (covalent) #status predicted.
F;2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pr: F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental F;5625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental F;2634,2802,2804/Disulfide bonds: interchain #status predicted
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F;327-413/Domain: fibronectin type III repeat homology <FN2>
F;414-502/Domain: fibronectin type III repeat homology <FN3>
F;508-593/Domain: fibronectin type III repeat homology <FN4>
F;508-683/Domain: fibronectin type III repeat homology <FN5>
F;508-683/Domain: fibronectin type III repeat homology <FN6>
F;686-771/Domain: fibronectin type III repeat homology <FN7>
F;6862/Domain: fibronectin type III repeat homology <FN9-
F;776-862/Domain: fibronectin type III repeat homology <FN9-
F;864-952/Domain: fibronectin type III repeat homology <FN9-
F;864-952/Domain: fibronectin type III repeat homology <FN8-
F;954-1045/Domain: fibronectin type III repeat homology <FN8-
F;1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>
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A;Residues: 2395-2871, 'S',2873-2944 <RE2>
A;Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
R;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a A;Reference number: A55255; MUID:94224777; PMID:8170945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1170-1172/Region: cell attachment (R-G-D) F;1189-1253/Region: cysteine/proline-rich F;1254-2783/Region: interrupted helical F;1334-1336/Region: cell attachment (R-G-D) F;2008-2010/Region: cell attachment (R-G-D) F;2553-2555/Region: cell attachment (R-G-D)
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A;Note: defects in this gene can result in dominant and recessive A;Note: there are 118 introns
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Genet. 2, 273-278, 1993
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C;Function:
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A;Cross-references: GDB:128750; OMIM:120120
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Best Local :
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173 SILKKSC 179
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                                                                                                                                                                                                                 GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                                                                                                                                                                                     DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                      DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
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26.2%;
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Pred: No. 0.69;
7; Mismatches 83
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LVSRRVC

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A;Cross-references: GB.J00185; GB.J00186

A;Note: the authors translated the codon TAC at 519 as Thr; the 1 R;Mole, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.

J. Biol. Chem. 259, 3407-3412, 1984

A;Title: Complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete responsion.

A;Reference number: A20751; MUID:84161997; PMID:6546754

A;Accession: A00934

A;Molecule type: protein; mENA

A;Residues: 26-764 MOLD-

A;Cross-references: GB.K01566

A;Note: nucleic acid translation differs from the sequence shown A;Note: 736-Ser was also found

A;Note: 319cosylation sites were determined
                                                                                                                                                                                                                                                                                                                                                                                           A;Reference 339-509 <CAl>
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
R;Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human complement protein factor B gene: evidence A;Reference number: A25971; MUID:87102880; PMID:3643061
A;Accession: B25971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 260-296,'T','298-764 <CHR>
R;Campbell, R.D.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene coding for human complement
A;Reference number: A19947; MUID:83273641; PMID:6308626
A;Accession: A19947
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N,Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-
N,Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
C,Species: Homo sapiens (man)
C,Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C,Accession: S34075; A44622; A00934; A1918; A19947; B19947; B25971; S14339; A44628; I54
R,Mejia, J.E., Jahn, I., de la Salle, H.; Hauptmann, G.
Bubmitted to the EMBL Data Library, March 1993
A,Recession: S34075
A,Molecule type: mRNA
A,Residues: 1-764 <MEJ>
A,Residues: 1-764 <MEJ>
                                                                                                                                     Biochem. J. 274, 473-480, 19
A;Title: The principal site
A;Reference number: S14339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Christie, D.L.; Gagnon, J.
Biochem. J. 209, 61-70, 1983
A;Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of A;Reference number: A19188; MUID:83204002; PMID:6342610
A;Contents: the final paper in a series documenting the sequence, glycosylation site, A;Accession: A19188
                                 A; Molecule type: protein A; Residues: 270-329 < NIE>
                                                                                                           A; Accession: S14339
                                                                                                                                                                                                                                             R; Niemann, M.A.; Bhown, A.S.; Miller,
                                                                                                                                                                                                                                                                                      A; Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-99 < WUL>
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A;Title: Isolation of cDNA clones for the human complement protein factor B, a A;Reference number: A44622; MUID:83039428; PMID:6957884
A;Accession: A44622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:J00125
A;Accession: B19947
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A; Residues: 346-764 < CAM>
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A; Residues: 467-546; 550-595; 752-764 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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   site for carbohydrate
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                                                                                                                                     of glycation of human MUID:91174758; PMID:20
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lysine
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PMID:2006911
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under artificial conditions
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                                                                                                                                                                                                                                                                                   PID:g553534
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A;Status: transcar.
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-31,'Q',33-764 <RE2>
A;Residues: GB:L15702; NID:g291921;
Arross-references: GB:L15702; NID:g291921;
Arross-references: GB:L15702; NID:g291921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1-25/Domain: signal sequence #status predicted <SIGS
F;26-764/Product: complement factor B #status experimental <MATS
F;26-259/Product: complement factor B fragment #status experimental <BAFS
F;37-98/Domain: complement factor H repeat homology <FH1S
F;103-158/Domain: complement factor H repeat homology <FH2S
F;103-158/Domain: complement factor H repeat homology <FH2S
F;165-218/Domain: complement factor H repeat homology <FH3S
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBFS
F;268-458/Domain: von Willebrand factor type A repeat homology <VFAS
F;268-458/Domain: trypsin homology #status atypical <TRYS
F;37-75/Domain: trypsin homology #status atypical <TRYS
F;37-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Dif
F;122,142,265,378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-tys (complement factor D) #status experimental
F;526,576,699/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:BF
A;Cross-references: GDB:119726; OMIM:138470
A;Cross-references: GDB:119726; OMIM:138470
A;Map position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; 69:
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; 69:
A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor
C;Complex: complement factor C3/C5 convertase; Ba is released
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al A;Pathway: complement alternate pathway C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc C;Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic A; Reference number: I57824; MUID:94067177; PMID:8247029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689 R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanak Mol. Immunol. 30, 1587-1592, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alpha
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EMBO J. 3, 153-157,
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Best Local (
    147
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                                                                                                                                                                                                                                        328 DSSNADWVTKQLNEINYEDHKLKSGTNT-----KKALQAVYSMMSWPDDVPPEGWNRTR 381
                                                                                                                                                                                                                                                                                                                                                                                               270 NIYLVLDGSDSIGASNFTGAKKCLVNLIEKVASYGVKP--RYGLVTYATYPKIWVKVSEA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DLYFILDKSGSV-----LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE-
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LARIADSKDHVFPVNDGFQALQGIIHSILKKS
                                                                             HVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPREDYLDVYVFGVGPLVNQVNINA 441
                                                                                                                                                                                                                                                                                                             ---DREQIRQGLEEL----QKVLPGGDTYMHEGFERASEQIYYENR----
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22.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 105.5; D
Pred. No. 0.34;
                                                                                                                                                      ELHEDLFFYSEREANRSRDLGAIVYCVG--VKDFNETQ 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
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A,TILLE: Structure of cDNAs encoding the triple-helical domain of murine alpha-2(VI) col rate oligonucleotides for generation of novel cDNA clones.

A,Reference number: $13745; MUID:91226374; PMID:1709252

A,Accession: $13745; MUID:91226374; PMID:1709252

A,Accession: $13745; MUID:91226374; PMID:1709252

A,Nocle: the sequences: GBL:06343; NID:g192671; PIDN:AAA37441.1; PID:g192672

A,Note: the sequence from Fig. 3 is inconsistent with that from Fig. 4 in having 306-Ile
C,Superfamily: collagen VI; von Willebrand factor type A repeat homology
C,Keywords: alternative splicing; cartilage; cell binding; connective tissue; disulfide
F,12-28(Domain: signal sequence #status predicted <SIC>
F,29-1029/Product: collagen alpha 2(VI) chain #status predicted <MAT>
F,29-265/Domain: globular #status predicted <COL>
F,376-378/Region: cell attachment (R-G-D) motif
F,436-438/Region: cell attachment (R-G-D) motif
F,499-551/Region: cell attachment (R-G-D) motif
F,499-551/Region: cell attachment (R-G-D) motif
F,508-510/Region: cell attachment (R-G-D) motif
F,601-1029/Domain: yon Willebrand factor type A repeat homology <VWA3>
F,841-1012/Domain: yon Willebrand factor type A repeat homology <VWA3>
F,841-1012/Domain: yon Willebrand factor type A repeat homology <VWA3>
F,150,337,640,907,963/Binding site: carbohydrate (Asn) (covalent) #status predicted

CDL>
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C. Species: Mus musculus (house mouse)
C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: S21369 $28808; S13745; S18863
R; Ibrahimi, X.Y.Z.; Bardon, X.Y.Z.; Dani, C.
submitted to the EMBL Data Library, April 1992
A; Reference number: S21369
A; Reference number: S21369
A; Accession: S21369
A; Accession: S21369
A; Molecule type: mRNA
A; Residues: 1-1029 <IBR>
A; Cross-references: UNIPROT:Q02788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
R; Ibrahimi, A.; Bertrand, B.; Bardon, S.; Amri, E.Z.; Grimaldi, P.; Ailhaud, G.; Dani, C
Biochem. J. 289, 141-147, 1993
A; Title: Cloning of alpha2 chain of type VI collagen and expression during mouse develop
A; Reference number: S28808; MUID:93143659; PMID:8380980
A; Accession: S28808
A; Molecule type: mRNA
A; Residues: 266-1029 <IB2>
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
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Constantinou, C.D.; Jimenez, S.A.
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                                                                     162 DGFQALQGIIHSIL------KKSCIE 181
                                                                                                                                                                                                             109 DGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVN-----
                                                                                                                                                                                                                                                                                          116 EVFSPPGSDRASFTKSLQGIRSFRRG--TFTDCALANMTQQIRQHVGKGVVNFAVVI--T
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DSTEIDODTINRIIKVMKHEAYGECYKVSCLE 263
                                                                                                                                           DGHVTGSPCGGIKMQABRAREEGIRLFALAPNRNLNEQGLRDIANSPHELYRNNYATMRP 231
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1: uniprot_sprot:*
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O9h6x2 homo sapien
O9c252 mus musculu
P58335 homo sapien
O6dfx2 mus musculu
O8bbq8 halocynthia
O9qye7 rattus norv
O8t6u5 mytilus edu
O8t5c2 mytilus gal
O04588 eimeria max
O60847 mus musculu
P11215 homo sapien
O8c6k9 mus musculu
P11216 homo sapien
O8c6k9 mus musculu
P113194 gallus gall
O43981 eimeria ten
O9u8j9 neospora ca
O99715 homo sapien
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P20703 homo sapien
P207035 mus musculu
O13349 homo sapien
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111	111	111	111.5	112	112	113	113	113.5	114.5	114.5	114.5	116	116
11.8	11.8	11.8	11.8	11.9	11.9	12.0	12.0	12.0	12.1	12.1	12.1	12.3	12.3
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MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

AS trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

AS Alausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AN Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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AN Alleschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

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AN Alleschul M.J., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

AN ALLESCHIM, J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AN ARIONAS S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,

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AN ALLESCHIM, M.J., Woung A.C., Shevchenko Y., Bouffard G.G.,

AN Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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AN Allalon D.K., Muzny D.M., Green E.D., Dickson M.C.,

AN Allalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

AN Allalon D.K., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Tonc Marl Rad Sci II S. a 90:16809-16001/2002)
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Hillman R.T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
-1- FUNCTION: Cellular role is not yet known.
-1- SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis. Binding does not occur in the presence of calci
                                                                                 -I- TISSUE SPECIFICITY: Highly expressed in tumor endotheli-
but not in normal endothelial cells.
-I- DOMAIN: Binding to PA seems to be effected through the
-I- SIMILARITY: Belongs to the ATR family.
-I- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100;
Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.;
"Human capillary morphogenesis protein 2 functions as an anthra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequencing cDNAs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH ANTHRAX TOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type I ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                             Event-Alternative splicing; Named isoforms=4; Comment=Experimental confirmation may be lacking
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natl. Acad.
                                                                                                                                                                                                                                                                       IsoId=Q9H6X2-2; Sequence=VSP_000444, VSP_000445
                                                                                                                                                                                                                                                                                                                   IsoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low levels due to a premature codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                              IsoId=Q9H6X2-4;
                                                                                                                                                                                                                                 IsoId=Q9H6X2-3; Sequence=VSP_000446,
                                                                                                                                                                                                                                                                                                                                                                                                             isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a K., ...
Oyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36:40-45 (2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAT ARE
                                                                                                                                                                                         Sequence=VSP_000448, VSP_000449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99:16899-16903 (2002).
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Pfam; PF05586; Ant C; 1.
Pfam; PF00092; VWA; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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EMBL; AF421380; AAL26496.1; --
EMBL; AK025429; BAB15128.1; AL
EMBL; AK001463; BAA91707.1; AL
EMBL; BC012074; AAH12074.1; --
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CARBOHYD
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CHAIN
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EMBL; BC012074;
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                                                                                                                                                                        GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
                                                                                                    EREANRSRDLGAIVYCVGVKDENETQLARIADSKDHVEPVNDGFQALQGIIHSILKKSCI
                                                                                                                                           IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLPPYS
                                                                                          EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSCI
                                                                                                                                 IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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ilarity 100.0%;
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ALT_FRAME.
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Missing (In isoform
/FTId=VSP_000449.
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/FTId=VSP_000447.
DGSILAIALLILFLL -> LHKIASGPTTAACME
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Missing (In isoform 2).
/FTId=VSP 000445.
NEKPFSVEDTYLLCPAPILKEVGMKAALQV
                                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
                                                                                                                                                                                                               Score 943; DB 1;
Pred. No. 9.2e-73;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential) VWFA.
                                                                                                                                                                                                                                                                                              isoform 4)
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removed. Usage by ar
                                                                                                                                                                                                                                                                                                                          uT)
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STANDARD;

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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Basegawa Y., Nogami A., Schombach C., Gojobori T.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schriml L.M., Renapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gaseterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanal A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanal A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Kanal A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Kamachandran S.,
RA Wilming L.G., Wynshaw-Bortis A., Yanagisawa M., Yang I., Yang L.,
RA Venardo R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Venardo R., Wanshaw-Bortis A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Milming L.G., Wynshawa Y., Jarawa K., Arakawa T., Fukuda S.,
RA Milminshi A., Ysahino M., Waterston R., Lander E.S., Rogers J.,
RA Masanishi A., Sasaki N., Sasaki D., Shinagawa A.,
Tahalysis of the mouse transcriptome based on functional annotation of
RT 60,770 fill-length cDNAs ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60,770 full-length cDNAs.";
Nature 420:563-573(2002).
-!- FUNCTION: Cellular role is not yet known.
-!- SUBUNIT: Binds to the protective antigen
anthracis (By similarity).
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Anthrax toxin receptor 1 precursor (Tumor endothelial marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carson-Walter E.B., Watkins D.N., Nanda Kinzler K.W., St Croix B.;
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Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the ATR fami
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                           DOMAIN: Binding to PA seems (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                      Note=No experimental confirmation
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a license agreement (See http://www.isb-sib.ch/announce/
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Bell S.E., Mavila A., Salazar R., Bayless K.U., Ramayuru .., Maxwell S.A., Davis G.E.;

"Differential gene expression during capillary morphogenesis "Differential gene expression during capillary morphogenesis"
                                                                                                                                                                ATR2 HUMAN STANDARD; PRT; 489 AA PS8335; Q86UI1; Q8NB13; Q96NC7; 28-PEB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                                                                                    05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                            SEQUENCE
                                                                                                        Eukaryota; Metazoa;
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008400; Anth Ig.
InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
InterPro; IPR002035; VWF A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1916788;
                                              MEDLINE=21539596; PubMed=11683410;
                                                                                NCBI_TaxID=9606;
                                                                                              Mammalia; Eutheria;
                                                                                                                                Name=ANTXR2; Synonyms=CMG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                              (CMG-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PF05587; Anth Ic;
; PF05586; Ant C;
; PF00092; VWA; 1
                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                     100
                                                                                                                                                                                                                                                                          220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                          M)
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                                                                                                                                                                                                                                                                                                                                                                                                                                GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    IRQGLESLQKVLPGGDTYMHEGFERASEQIYYENSQGYRTASVIIALTDGELHEDLFFYS
                                                                                                                                                                                                                                                                                                                                                                                                                   GFDLYFILDKSGSVLHHWNEIYYFVEQLAHRFISBQLRMSFIVFSTRGTTLMKLTEDREQ
                                                                                                                                                                                                                                                                                                                        EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                                                                                                                                                                                                                                                                                                                                             EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI 180
                                                                                                                                                                                                                                                                                                                                                                                            IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS 120
                                                                                                                                                                                                                                                                                                181
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                                                                                                                   (Human)
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                                                           (ISOFORM
                                                                                              Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62308
                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 934; DB 1;
Pred. No. 5.5e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQAWMFSSFLERAFQ (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
GRCINFTRVKNSQPAKYPLNNTYHPSSPPPAPIYTPPPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anthrax toxin receptor 1. Extracellular (Potential).
                                                                                              Catarrhini;
                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP_000450.
6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCPPPAPSAPTPPIPSPPSTLPPPPQAPPPNRAPPPSRPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asp/Glu-rich
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                                                                                                Hominidae;
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                                                                                                                                                      morphogenesis protein-2)
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    basement
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RA SUGAWATA M., TakAnashi M., Kanda K., YOKOI T., FURLYA T., KIKGAWA E.,
RA OMULTA Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe M., Hara H., Tanase T.-O.,
RA Kusano J., Kanehori K., Takahashi-Pujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Kawabata A., Hikiji T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Kawabata A., Hikiji T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakagima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nokimara K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
"Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H. Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Isonagi T., Wagatsuma M., Sato K., Katuta Y., Kodaira H., Kondo H., Shiratori A., Sudo H., Kanda K., Yokoi T., Furuya T., Kikawa M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa M., Takahashi M., Kantara N., Sato K., Katuta N., Sato K., Kanihara K., Katuta N., Sato K., Kanihara K., Katuta N., Sato K., Tanikawa M., Yamanaki M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100; Scoble H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane matrix
differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Synovial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSUE=Placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Cellular role is not yet known.

SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the following preference: calcium > manganese > magnesium > zinc.

Seems to bind to collagen type IV and laminin.

SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmic reticulum and not at the plasma membrane.
IsoId=P58335-4; Sequence=VSP_008346;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in colon, heart,
liver, peripheral blood leukocytes, placenta, a
small intestine and spleen.
DOMAIN: Binding to PA seems to be effected thro
SIMILARITY: Belongs to the ATR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCE Event=Alternative
                                                                                                                                                                                                                                                                                                                                       Note=No
                                                                                                                                                                                                                                                                                                                                                                             IsoId=P58335-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P58335-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e matrix assembly, cell cycle progression, ntiation and G-protein signaling."; Sci. 114:2755-2773(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36:40-45(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRODUCTS
                                                                                                                                                                                                                                                                                                                              Sequence=VSP_008344, VSP_008
ental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence=VSP_008343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           splicing; Named isoforms=4;
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                                          through
                                                                                                                           skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cellular
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                                              the VWA domain
                                                                                                                       lung,
muscle,
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EMBL; AY233452,
R EMBL; AK055536; BAB702,
AK055536; BAB702,
AK051521; BAC03731.1;
AM01721; BAC03731.1;
AM01721; BAC03731.1;
AM01721; AM01722;
AM1722; AM1722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                         Q6DFX2;
25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
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DOMAIN
DOMAIN
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
               Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                        Name=Antxr2;
                                                                            Anthrax toxin
                                                                                                                                                                      Q6DFX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
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InterPro; IPR002035; VWF_A.
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PF00092; VWA; 1
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an email to license@isb-sib.ch).
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AAP04016.1;
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TLDUSVSFNGGKSVISGSLIVTATECSNGIAAI
VTQAGVKWHDLTHCTFGLSGSGDPPTSAS (in
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chi; Muridae; Murinae; Mus
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CRC64;
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A Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bultonenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bultonenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bultonenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malak J.A., Gunaratne P.H.,

Ra Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ra Pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ra Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Phey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ra Hilasoley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ra Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Panner R.J. Marya M.A.,

Panner S.J. Ma
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008400; Anth Ig.
InterPro; IPR008399; Anth C.
InterPro; IPR008399; Anth C.
InterPro; IPR002035; VWF A.
Pfam; PF05586; Anth Ig; I.
Pfam; PF05586; Anth Ig; I.
SMART; SM00327; VWA; I.
                                                                                                  Q8BVM2
Q8BVM2;
01-MAR-2003
01-MAR-2003
                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical Proline-rich region/von
Willebrand factor type A domain containing protein, full insert
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"Generation and initial analysis of and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2004) to the EMBL/GenBank/DDBJ
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Pred. No. 4e-3
32; Mismatches
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PRINTS; PRO0453; VWF.
SMART; SM00327; VWA;
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Mammalia; Eutheria; Rodentia;
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 PS50234; VWFA;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono n., Landachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE-Testis;

MEDLINB-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (Risa) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                              EMBL; AK077206; BAC36683.1; -
GO; GO:00016021; C:integral to membrar
GO; GO:0004872; F:receptor activity;
InterPro; IPR008400; Anth Ig.
InterPro; IPR008400; WF A.
Pfam; PF05887; Anth Ig; I.
Pfam; PF00092; VWA; I.
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                                                                                                                                                                                                                                                                                             Tomaru A., Toya T., Yasunishi A., Muramatsu M., Submitted (APR-2002) to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P., Hayashizaki Y.; "High-efficiency full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection,"; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ry full-length cDNA cloning.";
303:19-44(1999).
VWFADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
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                                                                                                                                                                                         IEA.
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Matches 52
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                            Miyazawa S., Azumi K., Nonaka M.;
"Cloning and characterization of integrin alpha solitary ascidian, Halocynthia roretzi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Hemocyte;
MEDLINE=21103187; PubMed=11160215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
SEQUENCE 64
                                                                                                                                                                        SIGNAL
                                                                                                                                                                                    PROSITE; PS50234; VWFA; 1. Cell adhesion; Integrin; S
                                                                                                                                                                                                              SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                    PRINTS; PRO1185; INTEGRINA. PRINTS; PRO0453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=HrITGA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Integrin alpha Hrl precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003
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                                                                                                                                                                                                                                                                             InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                      InterPro; IPR000413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                        30; GO:0007229;
                                                                                                                                                                                                                                                                                                                 GO:0016021; C:integral to membrane; IEA.
GO:0008305; C:integrin complex; IEA.
GO:0005515; F:protein binding; IEA.
GO:0007160; P:cell-matrix adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                     AB048261; BAB21479.1; -. P11215; 18HQ.
                61
                                                                                                                                                                                                                                                                  PF00092; VWA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                        Similarity
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                IRQGLEELQKVLPG---
                                        GFDLYFILDKSGSVLHHWNBIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIE
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1332 AA;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation updat
                                                                                            Conservative
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                                                                                        Pred. No. 0.00
4; Mismatches
                                                                                                 Score 146; Db 2,
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Pred. No. 9e-24;
                                                                                                                                             integrin alpha Hr1.
fW; OD9108D2B05CFFAB CRC64;
                                                                                                                                                                       Potential.
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-GDTYMHEGFERASEQIYYENRQGYRT----
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05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor.
                                                                                                                                                                                                                                                                                                                                                                               -:- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).
-:- SUBCELULIAR LOCATION: Type I membrane protein (By similarity)
-:- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrin I-domains do not undergo protease cleavage.
-:- SIMILARITY: Belongs to the integrin alpha chain family.
-:- SIMILARITY: Contains 7 FG-GAP repeats.
  TRANSMEM
DOMAIN
                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of blood-
                                                                                                                  PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                                    InterPro; IPRO00413; Integrin_alp
InterPro; IPRO02035; VWF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF000357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                           DOMAIN
                                                   Repeat; Signal;
SIGNAL 1
                                                                             PROSITE; PS00242; INTEGRIN_ALPHA; PROSITE; PS50234; VWFA; 1.—Calcium; Cell adhesion; Glycoprot
                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Itgad;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clearing lipoproteins from plaq
borne pathogens, particulate ma
from the blood (By similarity).
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1101
1122
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                                                                 Transmembrane
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1161
1100
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Rodentia;
                                                                                                                                                                                                              Integrin_alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a D, a novel beta 2 integrin.";
to the EMBL/GenBank/DDBJ databases.
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                                                                          Glycoprotein; Integrin; Magnesium; Receptor;
 Potential.
Cytoplasmic
                         Integrin alpha-D.
Extracellular (Potential)
                                                      Potential
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1 variant a.
Mytilus edulis (Blue mussel).
Eukaryots; Metazos; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI TaxID-6550;
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Q8T6U5;
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;

Sun C., Lucas J.M., Waite J.H.;

"Collagen-binding matrix proteins from elastomeric extrao byssal fibers";

Biomacromolecules 3:1240-1248(2002).

EMBL; AF414454; AAL83537.1; -.

GO; GO:0005138; F:structural molecule activity; IEA.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2003 (TrEMBLrel. 24, Last annotation
Proximal thread matrix protein 1b.
Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pter
Mytiloidea; Mytilidae; Mytilus.
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EMBL; AY053390; AAL17973.1; -.
GO; GO:0005198; F:structural molecul
InterPro; IPR002035; VWF_A.
Pfam; PF00092; VWA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                   Matrix protein. SEQUENCE 444
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SMART; SM00327; VWA; 2.
PROSITE; PS50334; VWFA; 2.
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DGQNNGHKS---
                                            DGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVNDGFQ
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PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTSSFN
                                                                                                                                                                                                                                                                                                   46;
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                                                                                                                                                                                                                                                                                              Score 139; DB 2;
Pred. No. 0.0012;
6; Mismatches 74;
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Pred. No. 0.0012;
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RESULT 11
Q0458
ID Q0458
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Best Local S
Matches 49
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Pfam; PF00092; VWA; 2.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
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01-JUN-2002
01-JUN-2003
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 SEQUENCE FROM N.A.
MEDLINE=93149203; PubMed=8426611; DOI=10.1016/0166-6851(93)90255-V;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
                                                                                                               Q04588 PRELIMINARY; PRT; 724 AA. Q04588; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Major antigen homologous sequence (emp100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Mytilus galloprovincialis (Mediterranean mussel).
Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                     NCBI_TaxID=5804;
                                                                                     Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                      Eimeria maxima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomacromolecules 3:1240-1248(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY053391; AAL17974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLMKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                            DYSSKADIKGAID----KVSPSIIGQTAIGDGLENARLEV-FPNRNGGGREEVQKVVILLT
                                                                                                                                                                                                                                                                                                                                                                                                      E--DREQIRQGLEELQKYLPG--GDTYMHEGFERASEQIYYENRQG---YRTASVIIALT
                                                                                                                                                                                                                                                                                                                                                                                                                                    DIAFVFDASSSINANNPNNYQLMKNFMKDIVDRFNKTGPDGTQFAVVTFADRATKQFGLK
                                                                                                                                                                                                                                                                                       ALQGIIHSILKKSÇI 180
                                                                                                                                                                                                                                                                                                                     DGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTSSFD
                                                                                                                                                                                                                                                                                                                                                DGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFFVNDGFQ 165
                                                                                                                                                                                                                                                              KLSKIMEDVVKLACM
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 136; DB 2; Pred. No. 0.0023; No. 0.0023; No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecule
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Best Local S
Matches 53
Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R.W., Olsen B.R., Nishimura I.;
"Structural variation of type XII collagen at its carboxyl-terminal NCI domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274:22053-22059(1999).
                                                                                                                                      AND ALLE-2.
STRAIN-C578L/6J; TISSUE-Skin fibroblast;
MEDLINE-99348349; PubMed-10419532; DOI-10.1074/jbc.
Kania A.M.. Reichenberger E., Baur S.T., Karimbux k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q60847; P70322;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
Collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants
collagen XII and their tissue-specific expression during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE CAIC_MOUSE
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SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
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HSSP; P07996; ILSL.
GO; GO:0008083; F:gr
                                                                                                                                                                                                                                                                                                                                                                                                                            development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J, and Swiss Webster; TISSUE-Skin
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Mammalia; Eutheria;
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Mus musculus (Mouse)
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InterPro; IPR000762; PTN MK.
InterPro; IPR000884; TSPI.
InterPro; IPR002035; VWF-A.
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                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGGVSSQINGIIKAAC
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPRO0816; Collagen.

R InterPro; IPRO0895; ConA like_lec_gl.

R InterPro; IPRO0895; FN III-like.

R InterPro; IPRO0895; FN III-like.

R InterPro; IPRO03129; TSP_N.

R InterPro; IPRO03129; TSP_N.

R InterPro; IPRO03129; TSP_N.

R InterPro; IPRO03129; TSP_N.

R InterPro; IPRO03129; TSP_N.

R Pfam; PPO09121; Collagen; 5.

R Pfam; PPO0921; VAN; 4.

R Pfam; PPO0921; VAN; 1.

R Pfam; PPO0923; VAN; 1.

R Pfam; PPO0923; VAN; 1.

R PART; SMO0060; FN3; 18.

SMART; SM000210; TSPN; 1.

R SMART; SM000210; TSPN; 1.

R SMART; SM00210;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U25652; AAA99719.1; ALT_SEQ.
EMBL; U57095; AAB07047.1; -.
HSSP; P18614; 1MHP.
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SYMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

SYMILARITY: Contains 18 fibronectin type III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COLI domain could be associated with the surface of the fibrils, and the COLZ and NC3 domains may be localized in the perifibrillar matrix (By similarity).

SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences (By similarity).
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PTM: 0-glyco
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Name=XIIA-2; Synonyms=ER#K;
IsoId=Q60847-2; Sequence=VSP_001151,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=4; Comment=The final tissue form of collagen XII homotrimers or any combination of the various
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Y: Highest expression
era, blood vessels, ar
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in tendons, perichondrium,
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29.5%;
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O-linked (Xyl. (Potential).
Score 134.5; D
Pred. No. 0.03;
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MEDLINE-88257215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;

Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;

"Amino acid sequence of the alpha subunit of human leukocyte receptor Mol (complement receptor type 3).";

J. Cell Biol. 106:2153-2158(1988).
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genomic organization and
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Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor Neutrophil adherence receptor).
Name=ITGAM; Synonyms=CD11B, CR3A;
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                                                                                                                                                                                                                                                                                                                  lez D.A., Smith T.F., Tenen D.G.;
llb gene and phylogenetic analysis of
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st early diversification during
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"Experimental support for a beta-propeller domain in integrin alphasubunits and a calcium binding site on its lower surface.";
Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).
-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles it is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-beptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kalley L.L., Mildner A.M., Moon J.B., Mott J.E., Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.; "Cation binding to the integrin CD11b I domain and activation aggregation."
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MEDLINE=95171458; PubMed=7867070; DOI=10.10.

A Rieu P., Arnaout M.A., Liddington the
                                                                                                                                                                                                                                                                                                                                                                                Oxvig C., Springer T.A.; "Experimental support fo
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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;
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MEDLINE=96363671; PubMed=8747460; DOI=10.1016/S0969-2126(01)00271-4;
Lee J.O., Banketon L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway fo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee J.O., Rieu P., Arnaout M.A., Li "Crystal structure of the A domain CR3 (CD11b/CD18).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
MEDLINE-95171458; PubMed-7867070; DOI=10.1016/0092-8674(95)90517-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arna "N-terminal sequence of human leukoyte glycoprotein across species and homology to platelet IIb/IIIa."; Biochim. Biophys. Acta 874:368-371(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
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                                with I domains do not undergo prote SIMILARITY: Belongs to the integrin SIMILARITY: Contains 7 FG-GAP repeasIMILARITY: Contains 1 VWFA domain.
                                                                                                 associates with beta-2.
SUBCELULIAR LOCATION: Type I membrane prote:
TISSUE SPECIFICITY: Predominantly expressed
granulocytes.
DOMAIN: The integrin I-domain (insert) is a
                                                                                                                                                                                      of fibrinogen gamma chain.
SUBUNIT: Heterodimer of an alpha
                DATABASE: NAME=PROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80:631-638(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ley C.S., Arnaout M.A.;
promoter of the CD11b gene directs
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NOTE=CD guide
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Todd R.F. III, Arnaout M.A.;
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                         PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct
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                                                                       SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
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           protein sequencing;
Repeat; Signal;
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CHAIN
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN fullength enriched library, clone: B330019B14 product: hypothetical willebrand factor type A domain containing protein, full insert
                                             STRAINE-C57BL/6J; TISSUB=Ovary;

MEDLINE-2049374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                   "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSI
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Ovary; MEDLINE=21085660; PubMed=11217851; RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Ovary;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lonal annotation of a full-length mouse cDNA collection.";
409:685-690(2001).
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RESULT 15
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AC P1394; Q04509;
AC P1.304 (Rel. 13, Cr)
DT 01-UNV-1990 (Rel. 35, La)
DT 25-OCT-2004 (Rel. 45, La)
DE Collagen alpha 1(XII) ch
GN Name=COLIZA;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Choi
OC Archosauria; Aves; Neogr
OC Gallus.
OX NCBI_TaxID=9031;
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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nohamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RA HSSP, P11215; IMF7.
RMGD, MGT. 944756 PACASTANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R SMART; SM00327; VWA; 6.
R SMART; SM00327; VWA; 6.
PROSITE; PS50234; VWFA; 6.
Hypothetical protein.
SEQUENCE 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                          Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
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Pfam; PF00092; VWA; 6.
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STRAIN=C57BL/6J; T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                KPDLGKAIENIRQM--GGNTNTGAALNFTLKLLQRAKKE----
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                                                                                                                                                                                                         STANDARD;
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a K., Akimura T., Arakawa T.,
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                                         Neognathae;
                                                            Chordata;
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, Last annotation u
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9; Mismatches
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                                           Craniata; Vertebrata; ; Galliformes; Phasian
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(Fibrochimerin)
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                                           Phasianidae;
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                                         Phasianinae;
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STRAIN-White leghorn;
MEDLINE-92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE-92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,
Nishida Y., Obara M., Kimata K.;
"The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifs, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp
                       <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The two splice variants of collagen XII Biochim. Biophys. Acta 1171:97-98(1992).
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Gordon M.K., Gerecke D.R., Dublet B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Type XII collagen. A large multidomain to type IX collagen.";
                - PTM: The triple-helica
each end.
- PTM: Prollines at the t
unit (G-X-Y) are hydro
- PTM: O-glycosylated; g
(By similarity)
- SIMILARITY: Belongs to
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                                                                                                                                              ligaments, perichondrium, and periosteum, al tissues containing type I collagen.

DOMAIN: This sequence defines five distinct helical domains (COL1 and COL2) and three no domains (NC1, NC2, and NC3).

PTM: The triple-helical tail is stabilized between the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of triple of the triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of tr
                                                                                                                                                                                                                                                                                    IsoId=P13944-2; Sequence=VSP_001148; TISSUE SPECIFICITY: Type XII collagen
                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or any
combination of isoform Long and isoform Short. Only isoform Long
is a proteoglycan. Isoform Long has more restricted expression
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atl. Acad.
                                                                                Prolines at the third position (G-X-Y) are hydroxylated in some
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  Belongs
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three nontriple-helical
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molecule with partial homology
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InterPro; IPR008160; Collagen.

R InterPro; IPR008985; ConA like_lec_gl.

R InterPro; IPR003961; FN_III_-like.

R InterPro; IPR003957; FN_III_-like.

R InterPro; IPR003129; TSP_N.

R InterPro; IPR003129; TSP_N.

R InterPro; IPR003129; TSP_N.

R Pfam; PP01391; Collagen; 4.

R Pfam; PP02310; TSP_N; 1.

R Pfam; PP02321; VMPA; 4.

R PFAm; PP00032; VMA; 4.

R PRNSITS; PM00327; VWA; 4.

R PROSITS; SM00327; VWA; 4.

R PROSITS; PS50833; VWPA; 4.

R PROSITS; PS50833; VWPA; 4.

R PROSITS; PS50234; VWPA; 4.

Alternative splicing; Cell adhesion; Collagen;

Hydroxylation; Repeat; Signal; Extracellular matrix; Glycoprotein;

Hydroxylation; Repeat; Signal; Extracellular matrix; Glycoprotein;

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EMBL; X61024; CAA43358.1; -.
EMBL; M17375; AAA48718.1; -.
EMBL; J05137; AAA48635.1; -.
EMBL; X67327; CAA47774.1; -.
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                                                                                   Contains 18 fibronectin type III domains. Contains 1 TSP N-terminal (TSPN) domain. Contains 4 VWFA domains.
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                                 V----RKAATVIQHSGFSVFVVGVADVDYNELAKIASKPSERHVFIVDD-FDAFEKIQDN 2499
                                                  LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHS
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Human polypeptide SEQ ID NO

2121.

22-OCT-2001 AAM38976;

(first entry)

AAM38976 standard;

protein;

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Zhou
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                                                  Novel nucleic acids and polypeptides, useful as central nervous system injuries.
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N-PSDB; AAIS8132.
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J, Zhao (
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Example 4; SEQ ID NO 2121; 10078pp; English.

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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing cameliorating symptoms of anthrax comprises a von Willebrand factor
                                                                                     WPI; 2003-720708/68
N-PSDB; ADI00557.
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(OKEE/)
(OZKA/)
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cutaneous; inhalation anthrax; human; TANGO 197 HisTag fusion; mutant;
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                                                                                                                                                                                                                                                                           (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 HiaTag fusion protein of the invention.
                         New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing ameliarating symptoms of anthrax comprises a von Willebrand factor domain (VWF) amino acid sequence and an amino acid sequence heteroto the VWF.
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to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003134786-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          von Willebrand
vWF amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TANGO197-His tag fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM64584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2001; 2001US-00038307
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                                                                                                                                                                           2003-829643/77.
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vWF.
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factor A-like domain amino acid sequence;
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No. 2.7e-92;
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Best Local
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              Novel nucleic acid sequences encoding TANGO-128, 140, 19 and 239 polypeptides useful for the treatment of asthma, arthritis, psoriasis and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                    TANGO: 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; prognosis systemic lupus erythematosus; transgenic animal; diagnosis; prognosis
                                                                                 WPI; 2000-465743/40.
N-PSDB; AAA47455.
                                                                                                                                                                                                                                                                     06-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TANGO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB01422 standard; protein; 333
                                                                                                                                                                                                  30-DEC-1998;
                                                                                                                                                                                                                                                                                                      WO200039284-A1
                                                                                                                                                                                                                                                                                                                                                                      prophylatic;
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                                                                                                                                  Holtzman DA;
                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                   23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
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                                                                                                                                                                                                                                                                                                                                                                        therapeutic; human.
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Pred. No. 2.7e-92;
; Mismatches 0;
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                              197, 212, 213,
ma, rheumatoid
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Best Local
                                 WPI; 2002-713235/77.
N-PSDB; ABV73883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyme's disease, cachexia and autoimmune diseases e.g. myssthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human anthrax toxin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP54905 standard; protein; 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases, rheumatoid arthritis, psoriasis, inflammatory bowel septic shock, ulcerative colitis, Crohn's disease, chronic myo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Fig 4; 209pp; English
                                                                                                                                                        05-DEC-2000; 2000US-0251481P
                                                                                                                                                                                                                                                              WO200246228-A2
                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  Anthrax; toxin; receptor; human; antibacterial.
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leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
                                                                                                                       (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                              Peptide
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Novel isolated polypeptide useful for identifying agent that prevents or

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Best Local
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                                                                                                                                             (ROTT/)
(OKEE/)
(OZKA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion; von Willebrand factor A-like domain; vWF; antibacterial; cutaneous; inhalation anthrax; human; TANGO 197.
  WPI; 2003-720708/68
                                                          Rottman
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                                                                                                                                                                                                                                                                                                                                                                                                                               US2003144193-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TANGO 197 protein.
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                                                                                                                                                                                                                                                             20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                               24-JUL-2002; 2002US-00201292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                             ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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Pred. No. 2.8e-92;
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RESULT 7

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                                                                                                                                                                                                        (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vWF amino acid sequence; anthrax; Bacillus anthracis; cu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the VWP. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation antibrax. The current sequence is that of the human
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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing ameliorating symptoms of anthrax comprises a von Willebrand factor
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Pred. No. 2.8e-92;
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                                                                                                                                              (ROTT/)
(OKEE/)
(OZKA/)
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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous
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DB; ADI00553.
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                                                                                                                             ) ROTTMAN J B.
) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
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Pred. No. 2.8e-92;
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                                                                                                    'n
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK B.
(HEAL/) HEALBY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 FLAG fusion protein of the invention.
                                                                                                         New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax; inhalation anthrax; human; TANGO197; FLAG; fusion protein; gene.
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ameliorating symptoms of anthrax comprises a vidomain (vWF) amino acid sequence and an amino

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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like
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Synthetic.
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plasmid pO
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DB; ADI00555.
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
                                                                                                                                                                 JB,
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:hrombin cleavage site and His tag"
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWP. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or amellorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 HiaTag fusion protein of the invention.
                       New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliareting symptoms of anthrax comprises a von Willebrand factor Adomain (WF) amino acid sequence and an amino acid sequence heterolog to the vWF.
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von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TANGO197-His tag fusion
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Best Local !
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Region
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                                                                                                                                                                                                                                                       Domain
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motif with amino
                                                                                                                                                                                                                                                                                                /note= "PA-binding fragment, begins at any amino acid in the range 27-43 and ends at any amino acid in the range 221-321, region specifically described in Claim 3"
                                                              motif with
                                                                                                            motif with
                                                                                                                                                       /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 52, 54, 118 and 150"
              /note= "forms metal ion-dependent adhesion site (MIDAS)
motif with amino acid residues 50, 52, 54 and 150"
                                                             /note= "forms metal ion-dependent
motif with amino acid residues 50,
                                                                                                                             /note=
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                                                                                                                                                                                                                                        notes
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                                                                                                                                                                                                                                                                      label
                                                                                                                                                                                                                                                                                                                                                                 label Signal peptide
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                                                                                                         "forms metal ion-dependent adhesion with amino acid residues 50, 54, 118
                                                                                                                                                                                                                                      "extracellular domain"
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Pred. No. 2.9e-92;
; Mismatches 0;
                                                                                                                                                                                                         domain"
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                                                             adhesion
, 52, 118
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                                                              and
                                                                                                            and
                                                                          site (MIDAS)
                                                                                                                          site (MIDAS)
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of a human surface-bound anthrax toxin receptor (ATR), as predicted from an isolated cDNA clone. Anthrax toxin protective antigen (PA) binds to the ATR at a von willebrand factor A domain located in the extracellular domain of ATR. The invention provides ATR polypeptides and polypucleotides, vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent that inhibits binding between PA and ATR at a level effective to reduce the severity of anthrax. Suitable agents include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at least 80% identical to these, a fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a monoclonal or
nucleic acid
   antibacterial; gene therapy;
                                                            TANGO197 extracellular domain-mutant
                                                                                                                     03-JUN-2004
                                                                                                                                                                                                                                     ADM64586 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human animal suffering from anthrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide useful for identifying agent that preveduces effect of anthrax toxin on host cell, for treating human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABV73881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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                                                                                                                     (first entry)
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Pred. No. 3.2e-92;
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uman or non-
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Best Local S
Matches 173
                              17-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 384
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                                                                                       AAE01439;
                                                                                                                                        AAE01439 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 44; SEQ ID NO 10; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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OZKAYNAK E.
HEALEY J J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 899; DB 7;
100.0%; Pred. No. 3.4e-92;
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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; organitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemocraxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene 4 encoded secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted protein; proliferative disorder; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abnormality;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developmental abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein HWLFR02,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorder;
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## Homo sapiens.

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Protein
                                          Peptide
             l.../
/label= Signal_peptide
                                           Location/Qualifiers
1. .27
/note= "Mature human secreted protein"
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# WO200134626-A1.

17-MAY-2001

01-NOV-2000; 2000WO-US030045

05-NOV-1999; 99US-0163581P. 30-JUN-2000; 2000US-0215133P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Komatsoulis GA, Moore PA, Birse É Z.

2001-308778/32.

New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives. and

Claim 11; Page 485-486; 562pp; English.

CC AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE0144-AAE01513 represent the proteins they encode. CC AAB01514-AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating cor ameliorating medical conditions, e.g., by protein or gene therapy. CC Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 28 genes, the new genes. Specific uses are described for each of the 28 genes, concert tumours, footal and developmental abnormalities, and include cdeveloping products for the diagnosis or treatment of proliferative cdisorders, cancer, tumours, footal and developmental abnormalities, community of the consistency of the consistency. The diseases of the immune system, AIDS, autoimmune consistency disorders (e.g., Alzheimer's disease, Parkinson's disease), constitute disorders, schizophrenia, asthma, skin disorders (e.g., considerative disorders, schizophrenia, asthma, skin disorders, constituted disorders, and consistency related disorders, and consistency and infections. The proteins can also be used to aid wound healing and epithelial cell coroliferation, to prevent skin aging due to sunburn, to maintain organs consistency, and in chemotaxis, and can be used as a food additive or an entrart ive to modify storage properties and inthodicas anecific for a consistency tive to modify storage properties. preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The represents a human secreted protein of invention

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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HAA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiintertility; antiintlammatory; antilicer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nouropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                             1; Page 874-875; 2102pp; English.
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                                                                                                                                                                                                                                                          schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                     ocal Similarity
 164
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                                                                         QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
              EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                                                                                                                                                                              403 AA;
EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                        QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                               DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
                                                                                                                                                                       Conservative
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                                                                                                                                                                                    Score 899; DB 5;
Pred. No. 3.7e-92
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Search completed: June 13, 2005, 19:56:53 Job time: 65.0514 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-485-618-37
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US-08-605-672-37
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US-09-193-043-37
US-09-193-618-52-55
US-08-485-618-55
US-08-482-293A-55
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### ALIGNMENTS

RESULT 1

US-08-286-889-37

Sequence 37, Application US/08286889 Patent No. 5470953

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GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                         Query Match 15.4%;
Best Local Similarity 28.3%;
Matches 52; Conservative 30
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
PILLING DATE: 23-DEC-1993
ATTORNEY/ACENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 138,659
REFERENCE/DOCKET NUMBER: 27866/32168
                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 TELEPAX: 312-474-0448
                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                     TELEFAX: 312-47
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CITY: Chicago
STATE: Illinois
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E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                               1151 amino acids
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                                                           36;
                                                         Score 138.5; DB 1;
Pred. No. 6.6e-07;
66; Mismatches 71;
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-37
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                                                                              Query Match 15.4%; Score 138.5; DB 1; Best Local Similarity 28.3%; Pred. No. 6.6e-07; Matches 52; Conservative 36; Mismatches 71;
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Patent No. 5728533
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
PRIOR APPLICATION NUMBER: US 08/362,652
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3279:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474.6300
                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino aci
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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CITY: Chicago
Illinois
Thited
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United
ZIP: 60606-6402
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142 DIAFLIDGSGSINGRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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amino acid
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233 South Wacker Drive, 6300 Sear Tower
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3239:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gallatin, m. mannica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
TITLE OF SEOUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS LENGTH: 1151 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-DEC-1993 PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illino
                                                                                                                                                                                                                                                                                                                                                              TYPE:
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TELEFAX: 312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States
114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 164
                                           202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                            142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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                                                                                  55 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 113
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// TOPOLOGY: linear
// MOLECULE TYPE: prot
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US-08-605-672-37
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Best Local Similarity
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRIOR DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
NEGISTRATION NUMBER: 38,659
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                  114 LPFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 164
                                                                       202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSÄKKILLVITDGQKYRD 256
                                                                                                                                             142 DIAFLIDGSGSINORDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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PLEYSDVI PAADKA---GIIRYAI GVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
                                                                                                          DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
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SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
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FILING DATE:
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23-DEC-19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Williams Jr., JOSEDH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312-474-0448
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                                                                                                                                             55 DREQIRQGLEBLOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 113
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GY: linear
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LQGI 168
                                    PLEYSDVI PAADKA---
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                                                                                                          DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
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28.3%; Pred. No. 6.6e-07;
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                                      -GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
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                                                                                                                                                                                                                                                                                                Length 1151;
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Patent No. 5837478
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/ACENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659

REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
313
                                    165 LQGI 168
                                                                        257 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
                                                                                                                                                    202 DPQSLVDPIVQLQ----
                                                                                                                                                                                                                            142 DIAFLIDGSGSINORDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
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                                                                                                          114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 164
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                                                                                                                                                                                                                                                                1 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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| LRSI 316
                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
GY: linear
LRSI 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1151 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                      15.4%; Score 138.5; DB 2; 28.3%; Pred. No. 6.6e-07; tive 36; Mismatches 71;
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                                                                                                                                                  -GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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                                                                                                                                                                                                                                                                                                                                          Length 1151;
                                                                                                                                                                                                                                                                                                        Indels
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR FILING DATE: 1993-12-23
PRIOR FILING DATE: 1993-12-23
PRIOR FILING DATE: 1993-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-688-307A-37; Sequence 37, Application US/09688307A; Patent No. 6432404
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gallatin, APPLICANT: Van der '
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EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, Micha APPLICANT: Van der Vieren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1998-11-16
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ORGANISM: Rattus rattus
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                                                                                        APPLICATION NUMBER: 08/286,889 FILING DATE: 1994-08-05
FILING DATE: 1994-12-21
APPLICATION NUMBER: 08/943,363
FILING DATE: 1997-10-03
                                                                APPLICATION NUMBER: 08/362,652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
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256

201 5 4 10;

Gaps

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GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915el Human 2
FILE REPERENCE: 27866/35004
CURRENT FILING DATE: 1999-07-08
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 09/173,497
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/443,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PACENTIN Ver. 2.0
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SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/09350259
Patent No. 6620915
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SOFTWARE: PatentIn Ver. 2.0
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LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 361
OTHER INFORMATION: Xaa = NAME/KEY: misc_feature
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LOCATION: 1117
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LOCATION: 506
OTHER INFORMATION: Xaa =
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LOCATION: 486
OTHER INFORMATION: Xaa =
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ORGANISM: Rattus rattus
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; TYPE: PRT ; ORGANISM: Rattus rattus US-09-350-259-37
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US-08-485-618-55
; Sequence 55, A
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GENERAL INFORMATION:
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Best Local Similarity 28.3%; Pred. No. 6.6e-07;
Matches 52; Conservative 36; Mismatches 71
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                              REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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CORRESPONDENCE ADDRESS:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
MOLECULE TYPE:
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CITY: Chicago
STATE: Illinois
                       TYPE: amino acid TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
                                                                                                                                                       TELEFAX:
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                                                                                                                                                         312-474-0448
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protein
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RESULT 11
US-08-362-652-55
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Query Match
Best Local Similarity 28.3
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 55, Application US/08362652 Patent No. 5766850
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

ATTORNEY/ACENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REGISTRATION NUMBER: 38,659
                                                                                                                                                                                               TELEPHONE: 312-474-630
TELEPAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                1161 amino acids
                                                                                                                                           linear
                                                                                                                                                                                                                                                                                     312-474-6300
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            15.4%; Score 138.5; DB 1; 28.3%; Pred. No. 6.7e-07; tive 36; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.4%; Score 138.5; DB 1; Length 1161; 28.3%; Pred. No. 6.7e-07; tive 36; Mismatches 71; Indels 25;
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                                                                                                                                                                                                                                                                                                                              27866/32391
                                                   Length 1161;
                 Indels
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                               Best Loc
Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 ami-
                                                  Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                   FILING DATE: 21-DEC-1994
ATTOKNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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PRIOR APPLICATION UNMBER: US 08/173,497
APPLICATION NUMBER: US 08/173,497
                                                                                                                                                                                                                                                                 TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 233 SC
CITY: Chicago
                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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                               52;
1 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                   Similarity
                                                                                                                                           amino acid
)GY: linear
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                                                                                                                                                                              1161 amino acids
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                                   Conservative
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                                                                                                                        protein
                                                  15.4%;
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cker Drive, 6300 Sear Tower
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                                   36;
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                                                                                                                                                                                                                                                                                                      27866/32684
                               Score 138.5; DB 2
Pred. No. 6.7e-07;
6; Mismatches 71
                                                                DB 2;
                                                                Length 1161;
                                 Indels
                               25;
                               Gaps
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US-08-482-293A-55
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                                                                                                                                                       US-08-482-293A-55
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GENERAL INFORMATION:
                                                                             Matches
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/286,889
PILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3268.
                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gallatin, W. Flactonica
APPLICANT: Van der Vieren, Monica
TTTLR OP INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-DEC-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/173,497
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                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                          TELEFAX: 25-3856
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
   152
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                                   1 plyfildksgsv-lhhwneiyyfveqlahkfispQlrmsfivfstrgttlmklte----
DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                        312-474-0448
                                                                           Conservative
                                                                                                                                                                     protein
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                                                                     15.4%; Score 138.5; DB 2;
28.3%; Pred. No. 6.7e-07;
28.3%; Mismatches 71;
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                                                                                                              Matches
                                                                                                                                                 Query Match
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
APPLICATION NUMBER: US 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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                                                                                                                                                                                                      MOLECULE TYPE: protein
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TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
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                                                                                                                               Local Similarity
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                        TBLEFAX:
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                                                                                                                                                                                                                                                             ENGTH:
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55 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 113
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                                   DIAFLIDGSGSINORDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
                                                                        DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE-----
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                                                                                                              Conservative
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21-DEC-1994
                                                                                                        15.4%; Score 138.5; DB 2
28.3%; Pred. No. 6.7e-07;
tive 36; Mismatches 71
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Sequence 55, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: WAN der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT PILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/962,652
EARLIER APPLICATION NUMBER: 08/962,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 55
LENGTH: 1161
TYPE: PAT
ORGANISM: Rattus rattus
Search completed: June 13, 2005, 20:05:09 Job time : 16.9024 secs
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US-09-193-043-55
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                              y Match 15.4%; Score 138.5; DB 3; Length 1161;
Local Similarity 28.3%; Pred. No. 6.7e-07;
hes 52; Conservative 36; Mismatches 71; Indels 25;
                                                                                    323 LRSI 326
                                                                                                                          165 LQGI 168
                                                                                                                                                                 267 PLEYSDVIPAADKA---GIIRYAIGYGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
                                                                                                                                                                                                  114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFVNDGFQA 164
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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              US-10-038-307-26

US-10-201-292-26

US-09-796-753-12

US-10-038-307-2

US-10-201-292-2

US-10-201-292-22

US-10-201-292-22

US-10-038-307-24

US-10-201-292-22

US-10-038-307-24

US-10-201-292-24
                                                                                                                                                                                                                                         Description
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Sequence 26, Appl
Sequence 12, Appl
Sequence 2, Appli
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Sequence
Sequence
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Sequence
Sequence
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2, Appli
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22, Appl
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9-79	04-047-2	-10-368-087-	-10-201-292-	-10-038-307-	-09-796-753-5	-10-201-292-	0-201-292-1	-10-201-292-1	-038-30	-10-038-307-1	-10-038-307-	-10-201-292-1	-10-038-307-1	-10-474-794-30	-10-474-	-09-918-715-30	-09-918-715-19	-09-833-245-6	-10-474-794-23	-10-474-794-18	-10-408-765A-	-10-301-822-19	-10-201-292-2	-10-038-307-	-09-918-715-23	-09-918-715-1	-10-201-292-1	-10-038-307-1	-10-047-542-9	-10-201-292-3	-10-201-292-3	-10-20	0-201-292-3
e 54,	quence 26:	equence 16	equence 6,	equence 6,	equence 52,	equence 16	equence 14,	equence 10,	e 16,	equence 14	equence 10,	equence 12,	equence 12	equence 30:	e 19	equence 30:	e 19	equence 620	equence 23:	equence 18	equence 18:	equence 19	equence 20	equence 20	equence 23:	equence 18	equence 18	equence 18	equence 99	equence 36	equence 34	Sequence 32, Appl	equence 30,

### ALIGNMENTS

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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

ITILE OF INVENTION: Tango 197 and Tango 216 Com

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 328

TYPE: PAT

ORGANISM: Homo sapiens

US-10-038-307-26
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Best Local Similarity 100.0%; Pred. No. 1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/10038307
Publication No. US20030134786A1
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                               104
                                                                                                                                                                                                                         173;
121 EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
                                                                                       61 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
                                                                                                                                      44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR 103
                                                                                                                                                                1 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR 60
                                            QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                        DB 14; Length 328;
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RESULT 3
US-09-796-753-12
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                                                                                                                                    CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,
PRIOR APPLICATION NUMBER: 09/223,
PRIOR FILING DATE: 1998-12-30
PRIOR PRIOR PAPPLICATION NUMBER: 09/224,
PRIOR APPLICATION NUMBER: 09/224,
PRIOR APPLICATION NUMBER: 09/224,
PRIOR APPLICATION NUMBER: 09/259,
PRIOR APPLICATION NUMBER: 09/259,
PRIOR FILING DATE: 1999-03-06
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
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PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR PILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Appropriation No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEI
APPLICANT: Engin OZKAYNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: 09/
FILING DATE: 1999-06-30
APPLICATION NUMBER: 09/
                                                                       FILING DATE: 1999-0
APPLICATION NUMBER:
FILING DATE: 1999-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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VENTION: SECRETED PROTEINS AND USES THEREOF
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lo. US20030144193A1
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                                                                       1999-06-29
                                                                                                                       1999-06-18
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100.0%; Pred. No. 1e-86;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             09/259,388
                                                                                                                                                                                                                                                                                                                                                                                           09/223,546
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                                                09/345,464
                                                                                                                                              09/336,536
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                                                                                                09/342,687
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                                                                                                                                                                                                                                                                              US-10-038-307-2
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                       Sequence 2, Application US/10038307
Publication No. US20030134786A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
SEQ ID NO 12
LENGTH: 333
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Best Local (
                                                                                                                   APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-20 PRIOR APPLICATION NUMBER: 09/
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R APPLICATION NUMBER:
R FILING DATE: 1999-09
R APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 1999-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                121 EANRSRDIGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
                                                                                                                                                                                                                                                                                                                                             164 EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 216
                                                                                                                                                                                                                                                                                                                                                                                                              104 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 100.0%; al Similarity 100.0%; 173; Conservative 0
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Pred. No. 1e-86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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103

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RESULT 6
US-10-038-307-22
ISGQUENCE 22, Application US/10038307
SEQUENCE 22, Application US/10038307
Publication No. US20030134788A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: JUdith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION UNDER: US/10/038,307
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Sudith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-038-307-2
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  FastSEQ
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Windows Version 4.0
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 342
TYPE: PAT
ORGANISM: Homo sapiens
US-10-201-292-22
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               Sequence 24, Application US/10038307

Publication No. US20030134786A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Engin OZKANYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999
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Best Local Similarity
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LENGTH: 342
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CURRENT APPLICATION NUMBER: US/10/038,307
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ORGANISM: Homo sapiens
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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEPE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and FILE REFERENCE: 7853-253-99

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 345

TYPE: PRT
                                                                       RESULT 10
US-09-833-245-621
; Sequence 621, Applicat
; Publication No. US2004
; GENERAL INFORMATION:
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Matches
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 345
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Publication No. US20030144193A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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            APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF346PCT
CURRENT APPLICATION
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                                                                                              Application US/09833245
b. US20040010134A1
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NUMBER: US/09/833,245
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100.0%; Pred. No. 1.1e-86;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 35
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 93
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 38
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 621
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANALYSE APPLICANT: AND OZENTARY APPLICANT: APPLICANT: APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                  Matches 173;
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Best Local (
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                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                     104
                  121 BANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSIL 173
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164
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                                                                                                                                         44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
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                                                                                           QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
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                                                                     QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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No. US20030144193A1
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Pred. No. 1.6e-86;
D; Mismatches 0;
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Pred. No. 1.4e-86;
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RESULT 12 US-10-201-292-30

Sequence 30,

Application US/10201292

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RESULT 13
US-10-201-292-32
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SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 460
TYPE: PRT
CORGANIZM: Homo sapiens
US-10-201-292-30
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/ ORGANISM: Homo sapiens
US-10-201-292-32
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APPLICANT: Theresa L. O'KEEPE
APPLICANT: Theresa L. O'KEEPE
APPLICANT: Theresa L. O'KEEPE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEG ID NOS: 36
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
TYPES: DET
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Publication No. US20030144193A1
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                                                                                                                                                                                                                                                                                              Best Local Similarity
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APPLICANT: JUdith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
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                                                                                    104 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 216
                         EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSIL 173
                                                                                                                                                                              DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLKMSFIVFSTRGTTLMKLTEDREQIR
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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NOWBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SRQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 504
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; ORGANISM: Homo sapiens
US-10-201-292-36
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US-10-201-292-36
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US-10-201-292-34
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 529
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                                                                                                                                                                                                                             Matches 173;
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Best Local
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAE
APPLICANT: Engin OZKAYNAE
APPLICANT: Budith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
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                                                                                                                                                                                                                                                ocal Similarity
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EANRSRDLGAIVYCVGVKDENETQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
                                                                                     QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
                                                                                                                                                                      DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR 60
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                                                               QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 216
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                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                     100.0%; St., 100.0%; Pr
                                                                                                                                                                                                                           Score 899; DB 14;
Pred. No. 2e-86;
Mismatches 0;
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Db 164 EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 216 Search completed: June 13, 2005, 20:36:51 Job time : 56.4703 secs

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Minimum
Maximum
                                                                                                                                                                                                                                             Run
                                           Total number of hits satisfying chosen parameters:
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Perfect score:
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                                                                         283416 seqs, 96216763 residues
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                                                                                                                                                   DLYFILDKSGSVLHHWNEIY.....
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                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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                                              283416
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Post-grocessing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

| 1: | PIR | 79:\* | 1: | PIT1:\* | 2: | PIT2:\* | 3: | PIT3:\* | 4: | PIT4:\*

Database

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	ø	8	7	თ	ທ	4	w	N	_	Result No.
87	7	87.5	88	88	88	88.5		92.5	93	96.5	98.5	99	100	100.5	101.5	102	104.5	109	110	110	110	113.5	•	121.5	121.5	125	128.5	129.5	Score
9.7	9.7	9.7	9.8	9.8	9.8	9.8	10.2	0	10.3	10.7		11.0	11.1	11.2	11.3		11.6			12.2			13.4	13.5	ω	13.9	14.3	14.4	Query Match 1
710	418	341	1218	1018	917	932	1179	3137	3176	761	1029	698	460	567	764	2944	929	3051	1888	1857	1747	760	1153	1163	712	3124	1153	724	Length 1
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		hypothetical prote		collagen alpha 2(V	collagen alpha 2(V	inter-alpha-inhibi	integrin alpha-E c	collagen alpha 3(V	collagen alpha 3(V	complement factor	гg			hypothetical prote	complement factor	agen	type XII collagen	hypothetical prote	alpha 1	collagen alpha 1(X	collagen alpha 1(X	classical-compleme	leukocyte surface	cell surface glyco	=	ž	cell surface glyco	gen Em10	Description

cell surface glycoprotein CD11b precursor [validated] - human
N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Ma
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD)

## ALIGNMENTS

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RESULT
RWHU1B
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A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR3>
F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F;433-433/Domain: thrombospondin type 1 repeat homology <THR5>
F;433-433/Domain: thrombospondin type 1 repeat homology <THR5>
F;494-556/Domain: thrombospondin type 1 repeat homology <THR6>
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A;Title: Sequence of a major Bimeria maxima antigen homologous A;Reference number: A48569; MUID:93149203; PMID:8426611
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A; Residues: 1-724 < PAS>
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;Date: 01-Dec.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                107
                                                                                                                                                           114 LFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                  58 QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 113
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                                                                                                                                                                                                                                                                                                                          DVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDLSDSRA 106
                                                                                                                                                                                                                QNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDGA----
                                                                                                         ----SSRRSQTLSAAEKLKNRGVÍIVVLGVGTGVNSAECRSÍAGCDTSDTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 129.5; DB Pred. No. 0.002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
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A; Roccule type: mRNA
A; Residues: 9-1153 <HIC>
A; Cross-references; GB:JO4145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross-references; GB:JO4145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross-references; GB:JO4145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross-references; GB:JO4145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the CD11b gene and phylogenetic analysis of the N; Flittle: A, A6526
A; Marchigenetic analysis of the CD11b gene and phylogenetic analysis of the Mylogenetic analysis of the Mylogenetic analysis of the Mylogenetic analysis of the Mylogenetic CD11b gromoter.
A, Residues: 17-31 A, A, Colession: 152567; MUID:92144986; PMID:1346576
A, Title: Characterization of the myeloid-specific CD11b gromoter.
A, Molecule type: DNA
A, Residues: 17-93 A, Molecule type: DNA
A, Residues: 17-93 
A, Flexibles: CD11b gromoter.
A, Molecule type: DNA
A, Residues: 17-94 A, Molecule type: DNA
A, Molecule type: DNA
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A, Molecule type: DNA
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A;Cross-references: GB:Mi
C;Comment: A common beta
C;Genetics:
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R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: CDNA sequence for the alpham subunit of the human neutrophil adher A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218
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J. Cell Biol. 106, 2153-2158, 198

A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion
A;Reference number: A28915; MUID:88257215; PMID:2454931

A;Accession: A28915
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A;Title: Molecular cloning of the alpha-subunit of human and A;Reference number: A94193; MUID:88190151; PMID:2833753
A;Accession: A30892
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Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A;Title: The promoter of the CD11b gene directs myeloid-specific and developmentally A;Reference number: A41600; MUID:92073318; PMID:1683702
A;Accession: A41600
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A; Residues: 1-499,501-965,'p',967-1153 <ARN>
A; Residues: 1-499,501-965,'p',967-1153 <ARN>
A; Crose-references: GB: M18044; GB: J03270; GB: M19664; GB: X07421; NID: g186935; PIDN: AAA59.
A; Note: the authors translated the codon TAC for residue 1129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was confined the codon.
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A; Residues: 917-1042 < AR2>
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A; Residues: 1-11
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A; Residues: 1-9 <SHE>
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                                         GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219 beta chain (CD18) forms a heterodimer with this chai
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P.; Tenen,
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A;Accession: B34485
A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 2772-2792;2846-2873 <GOR2>
A;Residues: 2772-2792;2846-2873 <GOR2>
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA
A;Reference number: A28037; MUID:87317590; PMID:3476925
A;Accession: A28037
A;Molecule type: mRNA
A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-3124 <YAM'>
A;Residues: 1-3124 <YAM'>
A;Residues: 1-3124 <YAM'>
A;Residues: references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
A;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A;Title: Type XII collagen. A large multidomain molecule with partial homology to type I)
A;Reference number: A34485; MUID:90062079; PMID:2584192
A;Accession: A34485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: fibrochimerin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #Bequence revi
C;Accession: A40020; A34485; E3448
C;Accession: A40020; A34485; E348
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F;17-1108/Domain: extracellular #status predicted <EXT>
F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F;465-473/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-601/Region: calcium/magnesium binding #status predicted
F;593-601/Region: calcium/magnesium binding #status predicted
F;593-601/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted <TMMD
F;1135-1153/Domain: intracellular #status predicted <INT>
F;865,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete primary structure of type XII collagen shows a chimeric molecule wi nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site. A;Reference number: A40020; MUID:92011862; PMID:1918137
A;Accession: A40020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811 R;Yamagats, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nish.
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A;Cross-references: GDB:120599; OMIM:120980
A;Map position: 16p11.2-16p11.2
A;Note: promoter contains a GATA motif and t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(XII) chain precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A40020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 VNDGFQALQGI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 DIAFLIDGSGSIIPHDFRRMKEFVST-----VMEQLKKSKTLFS-----LMQYSEEFRIH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTFKEFONNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGEKFGDPLGYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIÅSKPPRDHVFQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.3%;
ilarity 26.7%;
Conservative 3
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Pred. No. 0.0042;
8; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.; Nishida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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F;1-23; Joomain: signal sequence #status predicted <SIG>
F;1-23; Joomain: signal sequence #status predicted <SIG>
F;24-3124/Product: collagen alpha 1(XII) chain #status predicted <MATS
F;24-1199-3124/Product: collagen alpha 1(XII) chain #status predicted <MATS
F;24-105/Domain: Fibronectin type III repeat homology <FN3A>
F;24-105/Domain: von Willebrand factor type A repeat homology <VWA1>
F;137-301/Domain: fibronectin type III repeat homology <FN3B>
F;332-414/Domain: fibronectin type III repeat homology <FN3B>
F;332-414/Domain: von Willebrand factor type A repeat homology <FN3B>
F;629-1178/Domain: von Willebrand factor type A repeat homology <FN3C>
F;630-711/Domain: fibronectin type III repeat homology <FN3C>
F;630-711/Domain: fibronectin type III repeat homology <FN3G>
F;101-895/Domain: fibronectin type III repeat homology <FN3G>
F;995-1076/Domain: fibronectin type III repeat homology <FN3G>
F;1086-1169/Domain: fibronectin type III repeat homology <FN3G>
F;1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F;1197-1361/Domain: fibronectin type III repeat homology <FN3H>
F;1198-1361/Domain: fibronectin type III repeat homology <FN3H>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1384-2295/Domain: IIID #status predicted <!IID>
F;1384-1465/Domain: fibronectin type III repeat homology <FN3I>
F;1384-1465/Domain: fibronectin type III repeat homology <FN3I>
F;1474-1557/Domain: fibronectin type III repeat homology <FN3K>
F;1566-1647/Domain: fibronectin type III repeat homology <FN3K>
F;1655-1738/Domain: fibronectin type III repeat homology <FN3N>
F;1647-1298/Domain: fibronectin type III repeat homology <FN3N>
F;1847-1298/Domain: fibronectin type III repeat homology <FN3O>
F;1937-2019/Domain: fibronectin type III repeat homology <FN3O>
F;1937-2019/Domain: fibronectin type III repeat homology <FN3O>
F;2119-2199/Domain: fibronectin type III repeat homology <FN3O>
F;2119-2199/Domain: fibronectin type III repeat homology <FN3O>
F;2119-2199/Domain: fibronectin type III repeat homology <FN3O>
F;2139-2294/Domain: fibronectin type III repeat homology <FN3O>
F;2325-2494/Domain: fibronectin type III repeat homology <FN3O>
F;2325-2494/
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A,Residues: 1-24,1189-1257,'8',1259-1263,'E',1265-1280
A,Cross-references: EMBL:X67327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 262, 17724-17727, 1987
A,Title: Type XII collagen is expressed in A,Reference number: S22254, MUID:88087065,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
R;Dublet, B.; van der Rest, M.
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A,Title: The two splice variants of collagen XII share a common
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;2946-3048/Domain:
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A,Accession: S28811
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                                                                                                                                                                                                                                                                                                                                                                                                                       72903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
72946-3048/Domain: collagenous COL1 #status predicted <CCL1>
73049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
73049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
730,106,1032,1044,1512,1767,2210,2273,2532,2683/Binding site:
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,Residues: 2831-2832,'T',2834,'R',2836-2843,3002-3014 <DUB>
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                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline
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                                                                                                                                                                                                                         Similarity
DLYFILDKSGSV-LHHWNBIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLMKLT--E 54
                                                                                                                                                                       Conservative
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splicing; cell binding; coiled coil; connective t
                                                                                                                                                                                                              13.9%; Score 125; DB 2
27.1%; Pred. No. 0.028;
                                                                                                                                                                       Mismatches
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PMID:3121603
                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                            74;
                                                                                                                                                                                                                                                                      Length 3124;
                                                                                                                                                                       Indels 16;
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1163 <COR>
A; Cross-references: UNIPROT: P20702
A; Note: this revision to the sequence from reference A35543 includes
A; Note: this revision to the sequence from reference A35543 includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:043981; GB:AF032905; GB:M73495; NID:g2707732; A;Note: sequence extracted from NCBI backbonne (NCBIN:77752, NCBIP:77756) F;48-218/Domain: von Willebrand factor type A repeat homology <VWA1> F;238-296/Domain: thrombospondin type 1 repeat homology <THR1> F;309-371/Domain: thrombospondin type 1 repeat homology <THR2> F;372-432/Domain: thrombospondin type 1 repeat homology <THR3> F;434-493/Domain: thrombospondin type 1 repeat homology <THR4> F;434-493/Domain: thrombospondin type 1 repeat homology <THR5> F;494-556/Domain: thrombospondin type 1 repeat homology <THR5> F;494-56/Domain: thrombospondin type 1 repeat homology <THR5> F;496-610/Domain: thrombospondin type 1 repeat homology <THR6>
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A45638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Tomley, F.M.; Clarke, L.B.; Kawazoe, U.; Dijkema, R.; Kok, J.J. Mol. Biochem. Parasitol. 49, 277-289, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064; PMID:1775171
A;Accession: A45638
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit,
A;Reference number: A35543; MUID:90153906; PMID:2303426
                                                                                                                                                                                                                                                                                               A;Reference number: A36584
A;Contents: erratum
                                                                                                                                                                                                                                                                                                                                                                    R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A. J. Biol. Chem. 265, 12750-12751, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues:
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C;Species: Eimeria tenella
C;Jate: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                            ;Species: Homo sapiens (man)
;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004;Accession: A35584; A35543; S00864
                                                                                                                                                                                                                                                                       Accession: A36584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIRQGLEELQKVLPG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V----RKAATVIQHSGFSVFVVGVADVDYNELAKIASKPSERHVFIVDD-FDAFEKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVRWNLSDPKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVMLVVDESGSIGTSNFRKVRQFIEDFVNSMPISPEDVRVGLITFAT------RS
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Pred. No. 0.0
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                                         leukocyte p150,95 molecule
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A;Gene: Mac-1

factor type A repeat homo.

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A;Molecule type: DNA
A;Residues: 1-1153 <PYT>
A;Residues: 1-1153 <PYT>
A;Cross-references: UNIPROT:P0555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Note: the authors translated the codon CAC for residue 569 as Gln
R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep
A;Reference number: I59078; MUID:86287312; PMID:2942940
A;Accession: I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukocyte surface glycoprotein Mac-1 alpha chain precursor - N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1999 #sequence_revision 30-Sep-1991 #text_charC;Accession: S00551; I59078
R;Pytela, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 16p11.2-16p11.2
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat h C;Superfamily: cell surface glycoprotein; heterodimer; magnesium; tandem repe F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F;20-1107/Domain: extracellular #status predicted <EXT>
F;20-119/Domain: von Willebrand factor type A repeat homology <VWA4>
F;1108-1133/Domain: transmembrane #status predicted <INT>
F;1108-1163/Domain: intracellular #status predicted <INT>
F;1134-1163/Domain: intracellular #status predicted <INT>
A; Cross-references:
                                 A;Molecule type: DNA
A;Residues: 11-44 <RES>
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A; Residues: 1-75,'L','757-1163 <CO3>
A; Residues: 1-75,'L','757-1163 <CO3>
A; Cross-references: GB: M81695; EMBL: Y00093; NID: g487829; PIDN: AAAB9180.1; PID: g487830
A; Note: part of this sequence was confirmed by protein sequencing
C; Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
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                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S00551;
A; Accession: S00551
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Amino acid
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                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND----IASKPSQEHIFKVED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPLSLLASVHQLQ-----GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIVFLIDGSGSISSRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEEFRRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
   GB:M14293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                   e of the murine MUID:88312584;
NID:g198993; PIDN:AAA39484.1; PID:g554193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMIM: 151510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 121.5; DB Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-Sep-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in reference A36584
K.; Larson, R.S.; S)
                                                                                                                                                                                                                                                                                                                                                                                                                   Mac-1 alpha chain
PMID:3044779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure of the alpha subunit PMID:3327687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               reveals homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of a leukocyt
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A;Molecule type: mRNA,
A;Residues: 660-677,'R',679,681-723,'G',725 <RES>
A;Residues: 660-677,'R',679,681-723,'G',725 <RES>
A;Cross-references: GB:M16271; NID:g199289; PIDN:AAA39562.1; PID:g199290
C;Genetics:
A;Introns: 16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1
C;Complex: The proenzyme forms a complex with C4a and is activated by cleavag C;Function:
A;Description: cleaves complement C3 and complement C5 alpha chains
A;Description: cleaves complement C3 and complement C5 alpha chains
A;Description: cleaves complement C3 and complement Factor H repeat homology; trypsin
C;Keywords: alternative splicing; complement classical pathway; duplication;
F;1-18/Domain: signal sequence #status predicted <SIG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-760 <ISH>
A;Residues: 1-760 <ISH>
A;Crose-references: EMBL:M57891; NID:g192436; PIDN:AAA63294.1; PID:g192437
A;Falus, A; Wakeland, E.K.; McConnell, T.J.; Gitlin, J.; Whitehead, A.S.;
R;Falus, E; Wakeland, E.K.; HcConnell, T.J.; Gitlin, J.; Whitehead, A.S.;
Immunogenetics 25, 290-298, 1987
Immunogenetics 25, 290-298, 1987
A;Title: DNA polymorphism of MHC III genes in inbred and wild mouse strains
A;Reference number: I54429; MUID:87192938; PMID:2883115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-760 <182>
A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1;
F;19-250/Product: complement C2b fragment #status predicted F;22-89/Domain: complement factor H repeat homology <FF1>F;94-149/Domain: complement factor H repeat homology <FH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: I54429
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; C
J. Biol. Chem. 265, 19040-19046, 1990
A;Title: Murine complement C2 and factor B
A;Reference number: A36593; MUID:91035430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993
C;Accession: A38876; B36593; T54429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A C;Keywords: cell adhaeion; glycoprotein; transmembrane protein F;1-16/Domain: signal sequence #status predicted <SIGS F;17-1153/product: leukocyte surface glycoprotein Mac-1 alpha chain #status F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2> F;1106-1129/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to GenBank, January 1991 A; Reference number: A38875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: B36593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: C3 convertase; C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           classical-complement-pathway C3/C5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 DIVFLIDGSGSI----NNIDF---QKMKBFVSTVMEQFKKSKTLFS----LMQYSDEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 27.2
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNDGFQALQGI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V-DNFEALNTI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGEKFGDPLDYKDVIPEADRA---GVIRYVIGVGNAFNKPQSRRELDTIASKPAGEHVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 120.5; DB 27.2%; Pred. No. 0.021; tive 34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               convertase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colten,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic and
PMID:2229060
                                                                                                                                                                                                                                                               290/3; 337/1; 384/1; 414/1; 461/1; th C4a and is activated by cleavage
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                                                       <C2B>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.S.; Colten,
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                                                                                                              homology; voglycoproteir
                                                                                                                                                                                                                                                            492/3; 53; into C2a,
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A;Molecule type: mRNA
A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest,
Eur. J. Blochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associate
A;Reference number: S17035; MUID:92037585; PMID:1935930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NyAlternate names: undulin
C;Specias: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; B30085; B22916; B17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, J. Biol. Chem. 268, 12177-12184, 1993
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F;251-760/Product: complement C2a fragment long form #status predicted <C2A>
F;251-605,613-760/Product: complement C2a fragment short form #status predicted <C2S>
F;259-449/Domain: von Willebrand factor type A repeat homology <VFA>
F;478-747/Domain: trypsin homology #status atypical <TRY>
F;478-747/Domain: trypsin homology #status atypical <TRY>
F;22-62,49-98,94-136,122-149,156-197,1182-210,470-590,499-515,593-609,647-674,685-715/Dif
F;27,117,297,340,474,478,663/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;514,570,689/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: embryo skin A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:133364,)
                                                                                                                                                                                                                                                                                                                                                        R;Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of A;Reference number: S22916; MUID:92339443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data A/Reference number: S30085 A/Accession: S30085
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A; Residues: 1472-1660 < APT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A45974; MUID:93280195; A;Accession: A45974
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A;Molecule type: mRNA
A;Residues: 1472-1659 <GOR1:
                                                                A; Accession: S17035
                                                                                                                                                                                                                                                                                          A, Status: preliminary
                                                                                                                                                                                                                                                                                                                             A, Accession: 822916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: UNIPROT: P32018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(XIV) chain precursor, short form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:X65122; NID:g62871; PIDN:CAA46238.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 --VIIALTDGELHEDLFFYSEREANRSRDLGAI-------VYCVGV------KDFNE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LGSKKDGERHAFILQDA-KALQQIFEHML 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHTITLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKELNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-----NRQGYRTAS---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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PMID:1339349
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                                                                                                                                 fibril-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g938175
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                                                                                                                                                                                           der Rest, M.; Mayne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
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A,Molecule type: pro
A;Residues: 1551-15;
C;Keywords: alternal
F;40-204/Domain: vo
F;236-317/Domain: f
F;326-409/Domain: f
F;418-499/Domain: f
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S31212
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A; Molecule type: mRNA
A; Residues: 1-1857 <WAE>
A; Cross-references: EMBL: X70792; NID: g288874;
A; Cross-references: EMBL: X70792; NID: g288874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collagen alpha 1(XIV) chain precursor, short form - C;Species: Gallus gallus (chicken) C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #C;Accession: S31212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, Eur. J. Biochem. 212, 483-490, 1993
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F;924-1089/Domain: von Willebrand factor type A repeat homology
F;1111-1152/Domain: non-collagenous NC2 #status predicted <NC4>
F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>

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F;741-823/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete primary structure of chicken collagen A;Reference number: S31211; MUID:93185668; PMID:8444186
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F;716-798/Domain:
                                                                                                                                                                                                                                                                                                                                                                       ;1-28/Domain: signal sequence #status predicted <SIG>
;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted
;29-110/Domain: fibronectin type III repeat homology <FN3A>
;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
;352-433/Domain: fibronectin type III repeat homology <FN3B>
;442-525/Domain: fibronectin type III repeat homology <FN3B>
;534-614/Domain: fibronectin type III repeat homology <FN3B>
;623-707/Domain: fibronectin type III repeat homology <FN3E>
;633-707/Domain: fibronectin type III repeat homology <FN3F>
;741-823/Domain: fibronectin type III repeat homology <FN3F>
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NyResidues: 1551-1570;1593-1599;1639-1667 <GOR2>
NyResywords: alternative splicing; coiled coil; extracellular nyReywords: alternative splicing; coiled coil; extracellular nyReywords: alternative splicing; coiled coil; extracellular nyReywords: fibronecttin type III repeat homology <FN3B>
1236-409/Domain: fibronectin type III repeat homology <FN3C>
1418-498/Domain: fibronectin type III repeat homology <FN3C>
15507-591/Domain: fibronectin type III repeat homology <FN3E>
1625-707/Domain: fibronectin type III repeat homology <FN3E>
1625-707/Domain: fibronectin type III repeat homology <FN3E>
                                                                                                                                                     Matches
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                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                               922-1009/Domain:
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                                                                                                                                                                                                                                                                                                          1040-1205/Domain:
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                                                                                                                                                                                         Local
1042 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 110:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                986 TKETLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEAGMRKGIPKVLVVITDGRSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     926 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 112
                                                                                                                                                     48;
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                                                                    DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
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                                                                                                                                                                                                                                                                                                      fibronectin type III repeat von Willebrand factor type
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                                                                                                                                             Score 110; DB:
Pred. No. 0.3;
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 110; DB 2;
Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAA50063.1; PID:g288875 to the EMBL Data Library, Ja:
                                                                                                                                                                                                                                                                                                  homology
A repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular matrix; glycoprotein;
                                                                                                                                                                                                                          <u>ب</u>
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                                                                                                                                                     74;
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                                                                                                                                                                                                                              Length 1857;
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                                                                                                                                                                                                                                                                                                                                                   <FN3H>
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A;Gene: Coll4Al

C;Keywords: alternative splicing; coiled coil; extracellular matrix; glyco
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glyco
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glyco
F;29-1880 Product; collagen alpha liXIV) chain, long form #status predicts
F;29-110/Domain: fibronectin type III repeat homology <PN3As
F;156-320/Domain: fibronectin type III repeat homology <PN3Bs
F;442-525/Domain: fibronectin type III repeat homology <PN3Ds
F;442-525/Domain: fibronectin type III repeat homology <PN3Ds
F;632-07/Domain: fibronectin type III repeat homology <PN3Bs
F;623-707/Domain: fibronectin type III repeat homology <PN3Fs
F;632-914/Domain: fibronectin type III repeat homology <PN3Fs
F;332-914/Domain: fibronectin type III repeat homology <PN3Fs
F;922-1009/Domain: fibronectin type III repeat homology <PN3Hs
F;1040-1205/Domain: von Willebrand factor type A repeat homology <PN3Hs
                                          hypothetical protein T20G5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #t. C;Accession: S42373 R;Smith A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1888 <TRU>
A;Cross-references: UNIPROT:P32018; EMBL:X70793; NID:9288872
A;Cross-references: UNIPROT:P32018; EMBL:X70793; NID:9288872
B;Maelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.;
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31211
A; Reference number:
                                                                                                                                                                    RESULT 11
S42373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416;1460-1811,1843-1888
A;Cross-references: EMBL:X70793
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collagen alpha 1(XIV) chain precursor, long form - chicken C;Species: Gallue gallue (chicken) C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004 C;Accession: S78476; S31211 R;Trueb, B.
submitted to the EMBL Data Library,
A;Reference number: S42368
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                                                                                                                                                                                                                                                                                                          113 DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI
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                                                                                                                                                                                                                                                                  DV----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKETLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEAGMRKGIPKVLVVITDGRSQD 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DV-----NKVSREMOLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKI 1211
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                        March 1994
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                                                                                       10-Nov-1995 #text_change 09-May-2004
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A54849
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A; Molecule type: DN
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N;Alternate names: procollagen alpha 1(VII) chain C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text_change C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, K.R. Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele A;Reference number: IS1027; MUID:95246925; PMID:7729585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type XII collagen alpha-1 chain - eastern newt (fragment) c;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-20 C;Accession: I51027 R;Wei, Y; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q91145; EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g63264
F;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1; F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1> F;754-793/Domain: fibronectin type II repeat homology <2F1> F;754-793/Domain: EGF homology <EGF>
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A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
C;Genetics:
                                                                                                            collagen alpha 1(VII) chain precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-929 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                               114 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI 172
                                                                                                                                                                                                                                                                                                                                                                          693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 DIVLLVDGSWSIGRPNFKIVRNFISRVVEVFDIGSDRVQIAVSQYSGDPRTEWQLNTHKT 692
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                                                                                                                                                                                                                                                                                                                                                                                                                               60 ROGLEELOKVLP---GGDTYMHEGFERASEQIYYENROGY----RTASVIIALTDGELHED
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Pred. No. 0.67
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104.5; I
Pred. No. 0.4;
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A;Molecule type: mRNA
A;Residues: 'RFR', 372-517,'DV', 520-540,'W', 542-1255 <RES>
A;Residues: 'RFR', 372-517,'DV', 520-540,'W', 542-1255 <RES>
A;Cross-references: GB:S51236; NID:g262308; PIDN:AAB24637.1; PID:g262309
A;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, J. Biol. Chem. 264, 3822-3826, 1999
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV coll.
A;Reference number: A30296; MUID:89139437; PMID:2537292
A;Accession: A30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 815-892, 'E', 894-1439 <PAR>
A;Residues: 815-892, 'E', 894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A;Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright,
J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion paraference number: I56328; MUID:93107742; PMID:1469284
A;Accession: I56328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g3R;Christiano, A.M.; Ryynaenen, M.; Uitro, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A/Title: Dominant dystrophic epidermolysis bullosa: identification A/Reference number: A55255; MUID:94224777; PMID:8170945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mol. Genet. 2, 273-278, 1993
A;Title: The carboxyl-terminal half of type VII collagen, A;Reference number: I48103; MUID:93271985; PMID:8499916
A;Accession: I84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E'; 2032, 'C', 2034-2041; A; Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991

A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gA;Reference number: S16316; MUID:91334380; PMID:1871109

A;Accession: S16316
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A;Residues: 'EFR',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C'
A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699
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J. Biol. Chem. 269, 20256-2026, 1994
A;Title: Cloning of human type VII collagen
A;Reference number: A54849; MUID:94327588;
                                                                                                                                                                                                                                                                                                   A;Gene: GDB:COL7A1; EBR1; EBD1; EB
A;Cross-references: GDB:128750; OMIM:120120
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A, Residues: 2395-2871, 'S', 2873-2944 <RE2>
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A; Residues: 1-2944 <C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
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;Cross-references: UNIPROT:Q02388; GB:L02870; NID:g987124; PIDN:AAA75438.1;
¡Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.S.
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F;331-Johnsain: Volumination to type A repeat homology <PNALS
F;321-318/Domain: fibronectin type III repeat homology <PNALS
F;327-411/Domain: fibronectin type III repeat homology <PNALS
F;414-502/Domain: fibronectin type III repeat homology <PNALS
F;508-593/Domain: fibronectin type III repeat homology <PNALS
F;508-683/Domain: fibronectin type III repeat homology <PNALS
F;508-683/Domain: fibronectin type III repeat homology <PNALS
F;706-682/Domain: fibronectin type III repeat homology <PNALS
F;706-771/Domain: fibronectin type III repeat homology <PNALS
F;705-1019/Domain: fibronectin type III repeat homology <PNALS
F;954-1045/Domain: fibronectin type III repeat homology <PNALS
F;954-1045/Domain: con willebrand factor type A repeat homology <PNALS
F;1170-1172/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cell attachment (R-G-D) motif
F;253-2555/Region: cell attachment (R-G-D) motif
F;208-2010/Region: cell attachment (R-G-D) motif
F;2784-2944/Domain: carboxyl-terminal monhelical #status predicted <NC2>
F;2784-2944/Domain: animal Kunitz-type proteinase inhibitor homology <BRISF,2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BRISF,2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BRISF,2876-2918-2818,2864,2667,2673/Modified site: 4-hydroxyproline (Pro) #status experimental
F;2625,2631/Modified site: carbohydrate (Lys) (covalent) #status experimental
F;2634-2802.2802.2804/Dismilfide bonds: interchain #status predicted
F;2167-2804-2804/Domain: carboxyl-terminal monhelical site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Modified site: carbohydrate (Lys) (covalent) #status experimental
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Best Local
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DLV---DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVND-FSILRTLL
                                                               DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 169
                                                                                                                                 GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                    TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE 112
                                                                                                                                                                                                                                                                DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
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26.8%;
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ype III repeat homology <FN2>
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Pred. No. 2.6;
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208
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A; Molecule type: mRNA
A; Residues: 467-546;550-595;752-764 < WOO>
A; Cross-references: GB:J00185; GB:J00186
A; Note: the authors translated the codon TAC at 519
R; Mole, J.E.; Anderson, J.K.; Davison, E.A.; Woods,
J. Biol. Chem. 259, 3407-3412, 1984
A; Title: Complete primary structure for the zymogen
A; Reference number: A20751; MUID:84161997; PMID:6546
A; Accession: A00934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339;
R;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
submitted to the EMBL Data Library, March 1993
A;Reference number: S34075
A;Accession: S34075
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                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN: R;Woods, D.B.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein
                                                                                                                                                                                                                                                                                              A;Reference number: A44622; MUID:83039428; PMID:6957884 A;Accession: A44622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-764 < MEJ>
A;Molecule type: protein; mRNA
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PMID:6546754
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olten, H.R.
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A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1; PIDR:R;Niemann, M.A.; Bhown, A.S.; Miller, E.J.

Biochem. J. 274, 473-480, 1991

A;Title: The principal site of glycation of human complement Fac A;Reference number: S14339; MUID:91174758; PMID:2006911

A;Accession: S14339

A;Molecule type: protein
A;Residues: 270-329 (NIE>
A;Note: binding site for carbohydrate to lysine under artificial R;Morley, B.J.; Campbell, R.D.

EMBO J. 3, 153-157, 1994

A;Title: Internal homologies of the Ba fragment from human compl A;Reference number: A44628; MUID:84158524; PMID:6323161

A;Accession: A44628
A;Cross-references: GDB:119726; OMIM:138470
A;Map position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1;
                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; I R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, Mol. Immunol. 30, 1367-1592, Mol. Immunol. 30, 167-1592, GDNA cloning, nucleotide: A;Reference number: I57824; MUID:94067177; PMID:8247029 A;Accession: I57824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Restdues: 16-225,'F', 227-259 <MOR>
A;Restdues: 16-225,'F', 227-259 <MOR>
R;Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties of a recombinant zymogen of th
A;Reference number: 154409; MUID:94041399; PMID:8225386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Wu, L.; Morley, B.J.; Campbell, R.D. cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human A;Reference number: A25971; MUID:87102880; PMID A;Accession: B25971
                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-31, 'Q', 33-764 <RE2>
A; Cross-references: GB:L15702; NI
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A;Residues: 339-509 <CAl>
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-764 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-99 < WUL>
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A; Residues: 346-764 < CAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Christie,
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                                                                                                       A;Gene: GDB:BF
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                                                                                                                                                            Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922 Comment: 292-Cys has a free sulfhydryl.
                                                                                                                                                                                                                                                                                           Statue: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB/EMBL/DDBJ
   390/1; 424/1; 470/1;
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   502/3; 542/1;
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, S.; Volanakis,
                                                                                                                                                                                                                                                                                                                                                                                    sequencing, phenotypic
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   593/2; 619/1;
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      652/3;
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A; Note: gene is located in the major histocompatibility complex,
C; Complex: complement factor B initially forms an inactive compl
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hypothetical protein C16E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te C;Accession: T28797 R;Geisel, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;37-98/Domain: complement factor H repeat homology <FH1>
F;103-158/Domain: complement factor H repeat homology <FH2>
F;165-218/Domain: complement factor H repeat homology <FH3>
F;165-218/Domain: complement factor H repeat homology <FH3>
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF>
F;268-458/Domain: von Willebrand factor type A repeat homology <VFA>
F;268-458/Domain: trypsin homology #status atypical <TRY>
F;37-76;62-98;103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Diff;122,142,285,378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Ly8 (complement factor D) #status experimental
                                         5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid
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A;Experimental source: strain Bristol N2; clone C16E9
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F;1-25/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                        A; Introns: 15/3; 77/3; 132/1; 185/3; 231/1; 271/2; 301/2; 430/3; 509/1
                                                                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                         A; Gene:
                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-567 < GEI>
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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                                                                                                  Matches
                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated
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                                                                                                                                                                                                                                                            CESP: C16E9.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 NIYLVLDGSDSIGASNFTGAKKCLVNLIEKVASYGVKP--RYGLVTYATYPKIWVKVSEA
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                                              1 DLYFILDKSGSVLHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFS--TRGTTLMKLTEDR
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                                                                                                                              Similarity
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DIGIIFDSSGSLEKNFQKQLAFAKQLVEQMPISDNATRVGIVQFAGKTKVRVLANFSQNK
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                                                                                                  Conservative
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                                                                                                                           11.2%; Score 100.5;
24.1%; Pred. No. 0.5;
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Pred. No. 0.59;
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Q8dgy6	Q63870	. Q75r52	Q8mvq1	Q7tqc3	P61622	P34576	Q65zc2	P32018		Q9es77	Q8c720	Q8cbt2	Q964n4
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## ALIGNMENTS

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RESULT 1
RA CHEMPROLETY JOURNAL TO SURJEY BOLLETON HOLD REAL TO SURJEY Y. NIGHIKAWA T., OTSUKIT T., Surjeyama T., Irie R., RA WARAMATSU A., HAYASHI K., SATO H., NAGAI K., Kimura K., Makita H., RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Sekine M., Obayashi M., Nishi T., Shibahara T., Nakamura Y. RA Nagahari K., Murakami K., Yasuda T., Isono Y., Nakamura Y. RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., RA Shiratori A., Sudo H., Hosoiri T., Kahu Y., Kodaira H., Kondo H., RA Shiratori A., Sudo H., Hosoiri T., Kahu Y., Kodaira H., Kondo H., RA Shiratori A., Sudo H., Hosoiri T., Kahu Y., Kodaira H., Kondo H., RA Shirata Y., Abe K., Ishibashi T., Yamashita H., Murakawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hosoira Y., RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., RA Nomiyama H., Satoh N., Takami S., Terashina Y., Sano S., Komai F., Hara R., Takeuchi K., Arita M., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Nomiyama H., Satoh N., Takami S., Terashina Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sujiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Sujiyama A., Takamoto M., Chmori Y., Ra, Yamazaki M., Hikija T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kamabata A., Hikijai T., Kobatake N., Itoh T., Shigeta K., Senba T.,
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Anthrax toxin receptor 1 precursor (Tumor endothelial marker
Name=ANTXR1; Synonyms=ATR, TEM8;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH ANTHRAX TOXIN. MEDLINE=21557240; PubMed=11700562; DOI=10.1038/n35101998; Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; "Identification of the cellular receptor for anthrax toxin."; Nature 414:225-229(2001).
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MEDILINE=20407466; PubMed=10947988; DOI=10.1126/science.289.5482.1197;
St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=14702039;
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Science 289:1197-1202(2000).
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad Sci H S. A 60.1600 1000.
      Hillman R.T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCHO08.1-RESEARCH008.16 (2004).
-!- FUNCTION: Cellular role is not yet known.
-!- SUBGUNIT: Binding does not occur in the presence of calcianthracis. Binding does not occur in the presence of calci-
-!- SUBCELULAR LOCATION: Type I membrane protein (Probable).
-!- ALTERNATIVE PRODUCTS:
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100; Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=14759258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete sequencing CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okumura K., Nac
Nakai K., Yada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mizushima-Sugano J.,
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                                                                              - TISSUE SPECIFICITY: He but not in normal end to but not in sinding to part of similarity: Belongs to SIMILARITY: Contains
                                                                                                                                                                                                                                                                                        Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                             Event-Alternative splicing, Named isoforms-4, Comment-Experimental confirmation may be la
                                                                                                                                                                                                                                                              IsoId=Q9H6X2-2; Sequence=VSP_000444,
                                                                                                                                                                                                                                                                                                             codon
                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9H6X2-1;
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                                                                                               =Q9H6X2-4; Sequence=VSP_000448, VSP_000449;
SPECIFICITY: Highly expressed in tumor endothelial cin normal endothelial cells.
Binding to PA seems to be effected through the VWA
ITY: Belongs to the ATR family.
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Oyama M., Hata H., Watanabe M., Komatbu T.,
Ugano J., Satch T., Shirai Y., Takahashi Y., Nakagawa K.,
Nayase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R
ada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
equencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acad.
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                                                                              Belongs to the ATR fami
Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOI=10.1186/gb-2004-5-2-r8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTHRAX TOXIN.
                                                                                                                                                                                                                                                                                                         2-1; Sequence=Displayed;
produced at very low levels due to a premature stop
mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 100:5170-5174(2003).
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                                                                                                                                                                                                                          Sequence=VSP_000446,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903 (2002)
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InterPro; IPR008399; Ant
InterPro; IPR002035; VWF
InterPro; IPR002035; VWF
Pfam; PF05587; Anth Ig; I
Pfam; PF05586; Anth C; 1
Pfam; PF00092; VWA; 1
SMART; SM00327; VWA; 1
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BC012074;
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HGNC:21014; ANTXR1.
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                                                                                                EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                                                                                     QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                           DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
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Conservative
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AAL26496.1;
BAB15128.1;
BAA91707.1;
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Cytoplasmic
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/FTId=VSP_000445.
NEKPPSVEDTYLLCPAPILKEVGMKAALQV
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/FTId=VSP 000448.
Missing (In isoform 4).
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Pred. No. 1e-69;
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B118A00AD5DF2233
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Wissing (in isoform 2).
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sequence up

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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Schrimi L.M., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schrimi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Saraji H., Fletchar C.F., Forrest A., Frazer K.S.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanaja A., Kawaji H., Marchionni L., McKenzie L., Miki H.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magjort D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Ponttus J.U., Qi D., Ramachandran S.,
RA Petrovsky N., Pillai R., Ponttus J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Taylor M.S., Teasdale R.D., Tomita M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Verardo R., Wanshw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Vann Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Minaing L.G., Wanshizaka Y., Jarawa K., Arakawa T., Fukuda S.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Manaishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Nanishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Nanishi A., Sakai K., Saka
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=21443268; PubMed=1159528;

Carson-Walter E.B., Watkins D.N., Nanda A.,

Kinzler K.W., St Croix B.;

"Cell surface tumor endothelial markers are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266; Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 88-562 FROM N.A. (STRAIN=C57BL/6J; TISSUE-Embryo
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (Mouse).
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SIMILARITY: Bel
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    AF378762;
AK013005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9CZ52-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBoId=Q9CZ52-2; Sequence=VSP_000450;
                                                                                                             s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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BAB28591.1; ALT_INIT
                                        AAL11999.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available;
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Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 171;
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InterPro; IPR008399; Ant_C.
InterPro; IPR002035; VWFFA.
Pfam; PF05587; Anth_Ig; I.
Pfam; PF05587; Anth_Ig; I.
Pfam; PF05586; Ant_C; 1.
Pfam; PF009092; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATT2 HUMAN STANDARD; PRT; 489 An.
ATT2 HUMAN STANDARD; PRT; 489 An.
P58335; Q86UI1; Q8NB13; Q96NC7;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE=21539596; PubMed=11683410;

Bell S.E., Mavila A., Salazar R., Bayless K.J., K

Maxwell S.A., Davis G.E.;

"Differential gene expression during capillary mo
collagen matrices: regulated expression of genes :

membrane matrix assembly, cell cycle progression,
differentiation and G-protein signaling.";

J. Cell Sci. 114:2755-2773(2001).
SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION TISSUE-Placenta;
TISSUE-Placenta;
MEDLINE-22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100;
Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternative SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=ANTXR2; Synonyms=CMG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1916788; Antxr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLYFILDKSGSVLHHWNEIYYFVBQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EANRSRDLGAIVYCVGVXDPNETQLARIADSKDHVFFVNDGFQALQGIIHSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGLEELQKVLPGGDTYMHEGFERASEQIYYENSQGYRTAS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLYFILDKSGSVLHHWNEIYYFVEQLAHRFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
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341
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358
501
164
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260
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477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                            (ISOFORM 1), AND INTERACTION WITH ANTHRAX TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562
319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 890; DB 1;
Pred. No. 6.3e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
GRCINFTRVKNSQPAKYPLNNTYHPSSSPPAFIYTPPPPAP
HCPPPAPSAPTPPIPSPPSTLPPPPQAPPPNRAPPPSRPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA
WMFSSFLERAFQ (in isoform 2).
/FTId=VSP_000450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular (Potential).

Potential
                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asp/Glu-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                             Bayless K.J., Kanagala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (highly acidic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       morphogenesis
                                                                                                                                                                                                              morphogenesis
es involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 562
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                                                                                                                                                                                           cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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                                                                                                                                                                                                                 basement
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RA Comura Y., Abe K., Kamihara K., Kateutta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matanabe T., Sudyama A., Takemoto M., Kawakami B.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsunara K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
T., Taka M., Matana T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
T., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M., Taka M.
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                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                      This SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human capillary receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=14702039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seems to bind to collagen type IV and laminin.

SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly sympacal mittle to the cell surface.
                                                     s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EWBI European Bioinformatics Institute. There are no restric by non-profit institutions as long as its content is iffed and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                                                                                                                                                       liver, peripheral wavelen.
small intestine and spleen.
DOMAIN: Binding to PA seems to be effected through the VWA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in colon, heart, liver, peripheral blood leukocytes, placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Genet. 36:40-45(2004). FUNCTION: Cellular role is not yet known.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T., Suzuki Y., Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           while isoform 2 is predominantly expressed reticulum and not at the plasma membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P58335-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P58335-4; Sequence=VSP_008346;
non-profit
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...Nishikawa T., Ots
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a license
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T., Ishii S.,
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muscle,
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SEQUENCE FROM N.A.

STRAIN-C57BL/6; TISSUB-Eye;

MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler |

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
VARSPLIC
                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                               Name=Antxr2;
                                                                                                                       Anthrax toxin
                                                                                                                                25-OCT-2004 (TrEMBLrel. 25-OCT-2004 (TrEMBLrel.
                                                                                                                                                     Q6DFX2;
25-OCT-2004
                                                                                                                                                                         Q6DFX2
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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                                                                                                    Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008399;
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PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                 61 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY233452;
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                     DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
                                                                                                                                                                                                                                           EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50234; VWFA; 1
                                                                                                                                                                                                                        EAKISRSLGASVYCVGVLDFEQAQLERIADSKEQVFPVKGGFQALKGIINSIL
                                                                                                                                                                                                                                                               KGLEDLKRVSPVGETYIHEGLKLANEQI--QKAGGLKTSSIIIALTDGKLDGLVPSYAEK
                                                                                                                                                                                                                                                                                                      DLYFVLDKSGSVANNWIEIYNFVQQLAERFVSPEMRLSFIVFSSQATIILPLTGDRGKIS
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                                                                                                                                                                                                                                                                                                                                                                                 357
489
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                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                         PRELIMINARY;
                                                                                                                      receptor
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BAC03731.1;
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53692
                                                                               Chordata;
Rodentia;
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/FTId=VSP_008345.
VCIWECIEKELTA -> GRCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform 2).
/FTId=VSP_008343.
TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-linked
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                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VSP_008346.
P -> A (in Ref. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anthrax toxin
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                    B9F679DB75B6E2B7
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                     519; DB 1;
No. 9.7e-37;
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RESULT S
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AC QBBV
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DE 1111
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Datchenko L., Marusins K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues G., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 103
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWP A.
Pfam; PP05587; Anth Ig; I.
Pfam; PP05586; Ant C; 1.
Pfam; PP00092; VWA; 1.
                                                                                                                                                                                                                                                                           Q8BVM2
Q8BVM2;
01-MAR-2003
                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical Proline-rich region/von
Willebrand factor type A domain containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                    SEQUENCE FROM N.A.
STRAIN=C578L/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636;
                                                                                                            Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC076595; AAH76595.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                   equence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGLEDLKAVKPVGETYIHEGLKLANEQI--QNAGGLKASSIIIALTDGKLDGLVPSYAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGLEBLOKVLPGGDTYMHEGFERASEQIYYENROGYRTASVIIALTDGELHEDLFFYSER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLYFVLDKSGSVANNWIEIYNFVHQLTERFVSPEMRLSFIVFSSQATIILPLTGDRYKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N
                                                                                                                                                                                                                                                                                                                                                                                                        EAKKSRSLGASVYCVGVLDFEQAQLERIADSKDQVFPVKGGFQALKGIINSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 AA; 53184 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acad.
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .A.
TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci.
                                                                                                             Rodentia;
                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%;
59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 517; DB 2; Length 48 Pred. No. 1.4e-36; Indels 1; Mismatches 37; Indels
                                                                                                          Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61A400D60BC8DE69 CRC64;
                    DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 487;
                                                                                                          Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
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Query Match
Best Local
   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itch M., Aizawa K., Nagaoka S., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Kegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (Rira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (Rira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (Rira) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                     EMBL; AK077206; BAC36683.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0004872; F:receptor activity; IEA. InterPro; IPR008400; Anth Ig. InterPro; IPR008400; WF Ā. Pfam; PF08587; Anth Ig. Pfam; PF08587; Anth Ig. I. Pfam; PF00092; VWA; I.
                                                                              Hypothetical SEQUENCE 6
                                                                                                                                   PRINTS; PR00453; VWF; SMART; SM00327; VWA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected
prepare full-length cDNA libraries for rapid discovery
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meth.
                                                                                                                PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Testis; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
TANALYSIS of the mouse transcriptome based o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length cDNAs.";
420:563-573(2002).
                   Similarity
                                                                              641 AA;
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                                                                                                                                                     VWFADOMAIN
                                                                          70415 MW;
                   38.7%;
30;
Score 348; DB
Pred. No. 9.8e-
30; Mismatches
                                                                            199E300730BC85E3 CRC64;
                   8e-22;
                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p Phase I & II Team;
on functional annotation
                                     Length 641;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata
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Gaps
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Best Local (
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GO; GO:0016021; C:int
GO; GO:0003055; F:int
GO; GO:00005515; F:px
GO; GO:0007160; P:cel
GO; GO:0007229; P:int
                                                                                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1185; INTEGRINA. PRINTS; PRO0453; VWFADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002035; VWF_A.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BPQ8;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21103187; PubMed=11160215;
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin alpha Hrl precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0016021; C:integral to membrane; IEA.
GO:0008305; C:integrin complex; IEA.
GO:0005515; F:protein binding; IEA.
GO:0007160; P:cell-matrix adhesion; IEA.
GO:00071299; P:integrin-mediated signaling pathway; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                adhesion;
  146 ARIA---DSKDHVFPVNDGFQALQGIIHSI 172
                                                                                                                                        244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
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                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00191; Int_alpha; 5.
SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                  QGLEELQKVLPG------GDTYMHEGFERASEQIYYENRQGYRT-----
                                                                                                                                                                                                                                             DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYLVLDKSGSVADNWIHIYSFAEGLVKKFTNPNLRISIITYSTEAEVILPLTSDSKEIN
                                                            KVIRDFDDAYIGNKOVLLLLIDGQAKDNKLILP--NANRLRNKGIATFAVGVGEYDISEL
                                                                                                                                                                                                                 DVLFVLDGSGSVGKNFDKVKDWVKNIT------AKLDIGKEIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAKKARRMGAIVYTVGVFMYSKQQLVNIAGDPDRCFGVDEGFSALEGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGII 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSLLVLKSIVPQGLTHMQKGLRKANEQIRKSTLGGRIVNSVIIALTDGLLLLKPYLDTME
                                                                                                -----ASVITALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL
                                                                                                                                                                                                                                                                                                                                                                       31
1332
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                Integrin; Signal; Transmembrane.
1 30 Potential.
                                                                                                                                                                                                                                                                                                                                                                         AΑ;
                                                                                                                                                                                                                                                                                                                                                                                         1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWFA; 1.
                                                                                                                                                                                                                                                                                           15.7%; Score 141; DB 2; Length 1332;
24.3%; Pred. No. 0.0023;
tive 34; Mismatches 59; Indels 6
                                                                                                                                                                                                                                                                                                                                                                       145851 MW;
                                                                                                                                                                                                                                                                                                                                                                       integrin alpha Hrl.
W; OD9108D2B05CFFAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
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                                                        DOMAIN
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                                                                                                                                                                                                                                   Repeat;
SIGNAL
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-:- SUBCELUULAR LOCATION: Type I membrane protein (By similarity).
-:- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-:- SIMILARITY: Belongs to the integrin alpha chain family.
-:- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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990YE7;

05-JUL-2004 (Rel. 44, Created)

05-JUL-2004 (Rel. 44, Last sequence up

05-JUL-2004 (Rel. 44, Last annotation
                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                         Calcium;
                                                                                                                                                                                                                                                                                           PROSITE; PS00242; INTEGRIN_ALPHA; 1. PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000413; InterPro; IPR002035;
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O'Brien M.M., VanderVi
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Mammalia; Eutheria;
                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01839; FG-GAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 KLIASGIDSIDRVFTVTD-FGELDSIVKSL
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                                                                                                                                                                                                                                                 Signal;
                                                                                                                                                                                                                                                                         Cell adhesion;
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                                                                                                                                                                                                                                                       Transmembrane
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Rodentia;
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                                                                                                                                                                                                                                                                     Glycoprotein; Integrin; Magnesium;
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Potential.
Cytoplasmic (
FG-GAP 1.
FG-GAP 2.
VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 5.
FG-GAP 7.
                                                                                                                                                                                              Extracellular (Potential).
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                                                                                                                                                                                                               Integrin alpha-D
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Q04588;
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Pfam; PF00
Pfam; PF00
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                                                          MEDLINE=93149203; PubMed=8426611; DOI=10.1016/0166-6851(93)90255-V; Pasamontes L.E., Hug D., Huembelin M., Weber G.; "Sequence of a major Eimeria maxima antigen homologous to the Eimeri tenella microneme protein Etpl10."; Mol. Blochem. Parasitol. 57:171-174(1993).

EMBL; M99058; AAA29076.1; -.

EIR; A48569; A48569.

HSSP; P07996; ILSL.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR000762; PTN MK.
InterPro; IPR000884; TSPI.
InterPro; IPR000884; TSPI.
InterPro; IPR0000883; TSPI.
InterPro; IPR0000884; TSPI.
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Eukaryota; Alve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 2
Major antigen homologous
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                         PF00090; TSP 1;
PF00092; VWA; 1
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       PR00453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alveolata;
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       VWFADOMAIN
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Last sequence update)
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Pred. No. 0.00
36; Mismatches
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GFFKR motif.
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01-OCT-1996 (Rel. 34, Last sequence up
05-OCT-2004 (Rel. 45, Last annotation
Integrin alpha-M precursor (Cell surfasubunit) (CR-3 alpha chain) (CD11b) (I
(Neutrophil adherence receptor).
Name=ITGAM, Synonyms=CD11B, CR3A;
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MEDLINE=88257215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;

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Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;

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leukocyte adhesion glycoprotein Mol: chromosomal localization
homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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SMART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 5.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 724 AA; 75808 MW;
                                                                                                                                               MEDIINE=93123748; PubMed=8419480; Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.; "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE=89098893; PubMed=2563162;
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(CD11b) (Leukocyte adhesion
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"Experimental support for a beta-propeller domain in integrin alpha-
subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998).

-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iC3b fragment of
the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
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MEDLINE-98362595; PubMed-9687375; DOI=10.1016/S09569-2126(98)00093-8;
Baldwin E. T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
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MEDLINE=96363671; PubMed=8747466; DON=10.1016/S0969-2126(01)00271-4;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
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MEDLLINE=95;71458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integral (CD11b/CD18).";
CR3 (CD11b/CD18).";
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MEDLINE=92144986; PubMed=1346576;
namerin A.G., Tenen D.G.;
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"The promoter of the CD11b gene directs myeloid-specific which promoter of the cD11b gene directs myeloid-specific developmentally regulated expression.";

Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structure 6:923-935(1998).
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Shelley C.S., Arn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hickstein D.D., Roth G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195; DOI=10.1073/pnas.95.9.4870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 17-31. MEDLINE=87076671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "cDNA sequence
                              granulocytes.
DOMAIN: The int
with I-domains
                                                                                                                        associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane
TISSUE SPECIFICITY: Predominantly expi
                                                                                                                                                                                                                      of fibrinogen gamma chain.
SUBUNIT: Heterodimer of an alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80:631-638(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding to the integrin
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  receptor indicates homology to integrin alpha subunits.";
l. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3:1333-1340(1995).
                          The integrin I-domain (insert)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1683702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        м.ј.,
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                                                                                                                            protein.
ressed in monocyteв
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                                                               a VWFA domain.
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entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                  J03925;
M18044;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA59544.1;
AAA59491.1;
AAA59903.1;
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         PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5
SMART; SM00327; VWA; 1.
                                                                                                                           PDB; 11
Genew;
                                                                                   InterPro;
                                                                                               88
                                                                           InterPro;
                                                                                               GO:0008305;
GO:0007155;
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                                             PF01839; FG-GAP; 3.
PF00357; Integrin_alpha;
PF00092; VWA; 1.
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NA5; X-ray;
HGNC:6149;
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PS00242;
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IPR002035; VWF_A.
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X-ray; 1/
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X-ray;
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AAB24821.1;
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A=140-335.

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                                           A Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R.W., Disen B.R., Nishimura I.;

"Structural variation of type XII collagen at its carboxyl-terminal T (1) domain generated by tissue-specific alternative splicing.";

L. J. Biol. Chem. 274:2263-2205(1999).

C -i- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).

-i- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences (By similarity).

Event=Alforeration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        CAIC MOUSE STANDARD; PRT; 31
060847; P70332;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence up
25-OCT-2004 (Rel. 45, Last annotation collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                STRAIN-C57BL/6J, and Swiss Webster; TISSUE-Skin; MEDLINE-96170761; PubMed-8601036; Boehme K., Li Y., Oh P.S., Olsen B.R.; "Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic
                                                                                                                                                                                                                                                                                                                                                                       Name=Coll2al;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50234; VWPA; 1.

3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
                                                                                                                                                                                                                                              development
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                    AND XIIB-
                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane.
                  ALTERNATIVE PRODUCTS:
Event—Alternative splicing; Named isoforms=4;
Comment—The final tissue form of collagen XII
Comment—The final combination of the various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
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IsoId=Q60847-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNDGFQALQGI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTFKEFQNNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIAFLIDGSGSIIPHDFRRMKEFVST----VMEQLKKSKTLFS-----LMQYSEEFRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGEKFGDPLGYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT
                                                                                                                                                                                                                                  204:432-445(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
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1152
                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 128.5; DB Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Integrin alpha-M.
                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                   SPLICING (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                3119
                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                              carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                               may contain
                                                                                                                                                                                                             (ISOFORMS XIIA-2
                                                                                                                                                                                                                                                                                                                    XIIA-1
                                                                                                                                                                                                                                                      embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                    R. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                       the
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 EMBL;
HSSP;
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
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DR SMART; SM00060; FN3; 18.

BR SMART; SM00060; FN3; 18.

BR SMART; SM000210; TSPN; 1.

BR SMART; SM002210; TSPN; 4.

BR SMART; SM00227; VWA; 4.

BR PROSITE; PS50853; FN3; 18.

BR PROSITE; PS50853; FN3; 18.

BR PROSITE; PS50853; FN3; 18.

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BR PROSIT
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InterPro; IPR008160; Colhagen.
InterPro; IPR00895; Cona like_lec_
InterPro; IPR003961; FN_III.
InterPro; IPR003957; FN_III-like.
InterPro; IPR003129; TSP_N.
InterPro; IPR002025; VWF_A.
InterPro; IPR002025; COLLAGEN; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 18. Pfam; PF02210; TSP N; 1. Pfam; PF00092; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Highest expression in tendons, perichondrium, skin, cornea, sclera, blood vessela, and periosteum.

DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are predominant at early stages (ED7 and 11); at later stages of development (ED15 and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice variant continues to be expressed in several tissues, even after birth. The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages of embryonic development (ED15 and ED17).

PTM: The triple-helical tail is stabilized by disulfide bonds at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
PTM: O-glycosylation of isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                each end (By similarity). Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=XIIB-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=XIIB-1;
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U57095; AAB07047.1; -.
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903; Sun C., Lucas J.M., Waite J.H.; "Collagen-binding matrix proteins from elastomeric extrao byssal fibers."; Biomacromolecules 3:1240-1248(2002).
EMBL; AY053390; AAL17973.1; -.
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DFOM: DFOMOO; VWA. 2
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                                                                                         MEDLINE=87317590; PubMed=3476925; Gordon M.K., Gerecke D.R., Oleen B.R.; "Type XII collagen: distinct extracellular matrix component by CDNA cloning."; Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
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Matrix protein
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SMART; SM00327; VWA; 2.
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Weognathae; Galliformes; Phasianidae; Phasianinae;
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VWF A.

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EMBL; D00824; BAA00701.1;
EMBL; K61024; CAA43358.1;
EMBL; M17375; AAA48718.1;
EMBL; J05137; AAA48635.1;
EMBL; X67327; CAA47744.1;
PIR; A40020; A40020.
HSSP; P56199; 1QC5.
                InterPro; IPRO08160; C
InterPro; IPRO08985; C
InterPro; IPRO03961; F
InterPro; IPRO03129; T
InterPro; IPRO03129; T
InterPro; IPRO02035; V
Pfam; PP01391; Collage
Pfam; PP00041; fn3; 17
Pfam; PP02210; TSP_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Large and small splice variants of collagen XII: differential expression and ligand binding.";

J. Cell Biol. 130:1005-1014(1995).

-I- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibriliar matrix.

-I- SUBUNIT: Trimer of identical chains each containing 190 kDa on nontriple-helical sequences.

-I- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;

Comment=The final tissue form of collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collagen XII may contain the collag
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 18 fibronectin type III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoid-Pl3944-2; Sequence=VSP 001148; TISSUE SPECIFICITY: Type XII collagen is present in t ligaments, perichondrium, and periosteum, all dense c tissues containing type I collagen.

DOMAIN: This sequence defines five distinct domains, helical domains (COL1 and COL2) and three nontriple-P domains (NC1, NC2, and NC3).

PTM: The triple-helical tail is stabilized by disulfi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interrupted helices (FACIT) family. SIMILARITY: Contains 18 fibronectin SIMILARITY: Contains 1 TSP N-termin
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PTM: O-glycosylated;
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                                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
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SMART; SM00210; TSPN; 1.

SMART; SM00227; VMA; 4.

PROSITE; PS50853; FN3; 18.

PROSITE; PS50854; VWFA; 4.

Alternative splicing; Cell adhesion; Collagen;

Alternative sequencing; Extracellular matrix; Glycoprotein;

Hydroxylation; Repeat; Signal; Structural protein.
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O-linked (Xyl...) (cho (Potential).
N-linked (GlCNAC...) (N-linked (GlCNAC
 Score 125; DB
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Potential.

Collagen alpha 1(XII) chain.

Pibronectin type-III 1.
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Cell attachment site (Potential).
N-linked (GlNNAc. .) (Potential).
O-linked (Xyl. .) (chondroitin su
                                                                                                                                                                                                                                                                                                                                                                                                                          Nonhelical region (NC2)
Triple-helical region (
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Triple-helical region (COL2)
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    .) (chondroitin sulfate)

    chondroitin

                        Length 3124;
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AC Q13349; Q15575; Q15576;
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41; Conservative
  Created)
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GO; GO:0008083; F:growth factor activity; IE;
InterPro; IPR001969; Pept Asp As.
InterPro; IPR000762; PTN MK.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR002035; VWF A.
Pfam; PP00090; TSP 1; 6.
PFINITS; PR00453; VWFADOMAIN.
PRINITS; PR00453; VWFADOMAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00209; TSP1; 6.
SMART; SM00209; TSP1; 6.
SMART; SM00209; TSP1; 6.
SMART; SM002109; TSP1; 7.
PROSITE; PS500141; ASP PROTEASE; UNKNOWN_1.
PROSITE; PS500141; ASP PROTEASE; UNKNOWN_1.
PROSITE; PS500141; ASP PROTEASE; UNKNOWN_1.
PROSITE; PS500141; ASP PROTEASE; UNKNOWN_1.
PROSITE; PS500141; ASP PROTEASE; UNKNOWN_1.
SEQUENCE 765 AA; 82880 MW; 9727838CC1FE80
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SEQUENCE FROM N.A.

MEDLINE=20183852; PubMed=10717300; DOI=10.1010,...

Lovett J.L., Howe D.K., Sibley L.D.;

Lovett J.L., Howe D.K., Sibley L.D.;

"Molecular characterization of a thrombospondin-related anonymous protein homologue in Neospora caninum.";

Darasitol. 107:33-43(2000).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Thrombospondin-related adhesive protein homolog.
Name=MIC2;
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Mol. Biochem. Parasitol. 107:3
Mol. Biochem. Parasitol. 107:3
EMBL; AF061273; AAF01565.1; -.
HSSP; P07996; 1LSL.
GO; GO:0008083; F:growth facto
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27.5%; Pro
ative 27;
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Pred. No. 0.03
27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -I- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood.

-I- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R. Grayson M.H., Bochner B.S., Gallatin W.M., Staunton I. "The leukcyte integrin alpha D beta 2 binds VCAM-1: binding interface between I domain and VCAM-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99059842; PubMed=9841932;
Graygon M.H., Van der Vieren M., Sterbinsky S.A., Michael Ga
Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and
a an alternative ligand for vascular cell adhesion molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE-96257236; PubMed-86666289; DOI=10.1016/0378-1119(95)00869-1; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding interface between I dome J. Immunol. 163:1984-1990(1999)
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Gene 171:291-294(1996).
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"Structural and functional characterization gene CD11d. Essential role of Sp1 and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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MEDLINE=20187620; PubMed=10722744; DOI=10.1074/jbc.275.12.8959;
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                                                                                                                                                                                                                              ASSOCIATES WITH Deta-2.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell

lines and subsets of peripheral blood leukocytes and strongly on

tissue-specialized cells, including macrophages foam cells within

atherosclerotic plaques, and on splenic red pulp macrophages.

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins

with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 1 VWFA domain.
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annotation update)
(Leukointegrin alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sterbinsky S.A., Michael Gallatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vazeux R.,
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Calcium; Cell adhesion; Glycoprot
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PRINTS; PR00453; VWFADOMAIN
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InterPro; IPR002035; VWF_A.
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Extracellular (Potential)
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